

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 5, 2005, 05:59:29 ; Search time 232 Seconds  
(without alignments)  
319.312 Million cell updates/sec

Title: US-09-196-161d-1

Perfect score: 558  
Sequence: 1 GAAQGEANGNQPFAANNAAR.....PGGEAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	395	2 Q27208	ICHMU
2	558	100.0	442	2 Q9XG22	ICHMU
3	222	39.8	460	2 Q962N5	ICHMU
4	221	39.6	468	2 Q9BMH3	ICHMU
5	95	17.0	614	2 Q4VM07	VIPLE
6	93.5	16.8	371	2 Q9GPD0	TETTH
7	93	16.7	548	2 Q9G045	GIALA
8	93	16.7	677	2 Q7M3R4	GIALA
9	88.5	15.9	305	2 Q9GPP2	TETTH
10	88.5	15.9	316	2 Q9GPP3	TETTH
11	87	15.6	724	2 Q7QTV1	GIALA
12	85.5	15.3	518	2 Q8GIR8	SYNP7
13	85.5	15.3	518	2 Q5N1J8	SYNP6
14	85	15.2	316	2 Q9GPP4	TETTH
15	85	15.2	536	2 Q7QSK6	GIALA
16	85	15.2	692	2 Q7Q073	GIALA
17	85	15.2	692	2 Q818W4	GIALA
18	84.5	15.1	245	2 Q7Q0C5	GIALA
19	84.5	15.1	2330	1 EGFL4	MOUSE
20	84.5	15.1	2386	1 EGFL4	HUMAN
21	83	14.9	1190	1 LAMC2	HORSE
22	81.5	14.6	814	2 Q7R1V1	GIALA
23	81	14.5	130	2 Q9B1K1	GIALA
24	81	14.5	1429	2 Q4UH00	THEAN
25	81	14.5	1827	2 Q8JHV6	BRARE
26	80.5	14.4	560	2 Q9U013	GIALA
27	80.5	14.4	2855	2 Q61D08	CAEBR
28	80	14.3	338	2 Q6EQJ7	ORYSA
29	80	14.3	1118	2 Q61B94	CAEBR
30	79.5	14.2	759	2 Q4SBL9	TETNG
31	79.5	14.2	874	1 EGFL4	RAT

32	79.5	14.2	1019	2 Q9NA40	CAEBL	Q9NA40 caenorhabdi
33	79	14.2	155	2 Q88B00	PSESM	Q88B00 pseudomonas
34	79	14.2	600	2 Q9PVX7	NAJNA	Q9PVX7 naja naja (
35	79	14.2	3333	1 LAMM3	MOUSE	Q61789 mus musculu
36	78.5	14.1	239	2 Q7R376	GIALA	Q7R376 giardia lam
37	78.5	14.1	821	2 Q8VPM9	9M1CC	Q8VPM9 micrococcus
38	78.5	14.1	1336	2 Q61UE2	CAEBR	Q61UE2 caenorhabdi
39	78	14.0	596	2 Q07317	GIALA	Q07317 giardia lam
40	78	14.0	833	2 Q6J288	ACACA	Q6J288 acanthamoeb
41	78	14.0	3718	1 LAMM5	MOUSE	Q61001 mus musculu
42	77.5	13.9	484	2 Q9SLG2	SHEEP	Q9SLG2 ovie aries
43	77.5	13.9	569	2 Q7QXT3	GIALA	Q7QXT3 giardia lam
44	77.5	13.9	573	2 Q9HWQ0	PSEAE	Q9HWQ0 pseudomonas
45	77.5	13.9	1997	2 Q81RM7	CHIRE	Q81RM7 chlamydomon

## ALIGNMENTS

RESULT 1					
ID	Q27208	ICHMU	PRELIMINARY;	PRT;	395 AA.
AC	Q27208;				
DT	01-NOV-1996	(Tremblrel. 01, Created)			
DT	01-DEC-2001	(Tremblrel. 19, last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, last annotation update)			
DE	Immobilization antigen precursor (Fragment).				
OS	Ichthyophthirius multifiliis (White spot) (Ich).				
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;				
OX	Ophryoglenina; Ichthyophthirius.				
RN	NCBI_TaxID=5932;				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Georgia;				
RX	MEDLINE=92335298; PubMed=1631132;				
RA	Clark T.G., McGraw R.A., Dickerson H.W.;				
RT	"Developmental expression of surface antigen genes in the parasitic ciliate Ichthyophthirius multifiliis.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:6363-6367(1992).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Georgia;				
RX	MEDLINE=93020590; PubMed=1383510;				
RA	Lin T.L., Dickerson H.W.;				
RT	"Purification and partial characterization of immobilization antigens from Ichthyophthirius multifiliis.";				
RL	J. Protozool. 39:457-463(1992).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Georgia;				
RA	Clark T.;				
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; M92907; AAC36158.1; -; mRNA.				
DR	PIR; A46031; A46031.				
DR	GO; GO:0005489; F:electron transporter activity; IEA.				
DR	GO; GO:0005506; F:iron ion binding; IEA.				
DR	GO; GO:0006118; P:electron transport; IEA.				
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.				
DR	PRINTS; PR00353; 4FE4SFRDOXIN.				
KM	Signal.				
FT	SIGNAL <1				
FT	CHAIN 2				
FT	NON TER 1				
FT	SEQUENCE 395 AA; 39567 MW; 68DA2C790E4FD393 CRC64;				
QY	1 GAAQGEANGNQPFAANNAARGICVPCQINRVGSVTNAGDIATATGCGSTGCPGTALDDG 60				
DB	37 GAAQGEANGNQPFAANNAARGICVPCQINRVGSVTNAGDIATATGCGSTGCPGTALDDG 96				



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DR EMBL: AF312775; AAC38107.1; -, mRNA.
SQ SEQUENCE 371 AA; 35175 MW; 5817EFC517DEAC CRC64;
Query Match 16.8%; Score 93.5; DB 2; Length 371;
Best Local Similarity 30.4%; Pred. No. 0.38;
Matches 41; Conservative 5; Mismatches 48; Indels 41; Gaps 6;

Oy 1 GAAGGANGNPFANNAARGICVPCQINRGVSTNAG-----DLA 41
Db 50 GACCKCPTGNISVAA-TASGTLVTSCTCND---TNAGLKADNSGCCCKANFYGTPNAVA 104
Oy 42 TLATGCGNOCPTGALDDGVTVDF-----DRSAAQCVCKKPNFYNGSGSPQG 88
Db 105 GGATGCC-TACTGTGASPAAGTAATVSCADNTNASKDNSGCC--CKANFYGTPNAVAG 160
Oy 89 EAPGVQVFAAGAAA 103
Db 161 GATGCTACPTGSAANA 175

RESULT 7
O9GQ45 GIALA
ID O9GQ45 GIALA PRELIMINARY; PRT; 548 AA.
AC O9GQ45-
DT 01-MAR-2001 (TREMBLrel. 16; Created)
DT 01-MAR-2001 (TREMBLrel. 16; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE Variant-specific surface protein M21-1 (Fragment).
GN Name=M21-1;
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mansouri M., Ey P.L.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF298862; AAC37862.1; -, Genomic_DNA.
DR HSSP; O16119; 1E2G.
DR InterPro; IPR006058; 2FE2S_fd_BS.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR SMART; SM00261; EGF; 2.
DR SMART; SM00261; FU; 4.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578FE4FDA0A2CF0E CRC64;

Query Match 16.7%; Score 93; DB 2; Length 548;
Best Local Similarity 28.6%; Pred. No. 0.64;
Matches 30; Conservative 6; Mismatches 37; Indels 32; Gaps 6;

Oy 5 GEANGNPFANNAARGICVPCQINRGVSTNAGDLA-----TLATQC----- 47
Db 273 GCTGNHTFVVGSTNQK-LCVPC-----GDTTNGVGLGNTCSSXTTCTKCDGYVDSGG 326
Oy 48 ---STQCTPTALDDGVTVDFDRSAAQCVCKKPNFYNGSGSPQG 89
Db 327 TVTCTACPGANC-----ATLCERYRKQCTTCKPGFLLKDS-SGE 365

RESULT 8
O7M3R4 GIALA
ID O7M3R4 GIALA PRELIMINARY; PRT; 677 AA.
AC O7M3R4;
DT 01-MAR-2004 (TREMBLrel. 26; Created)
DT 01-MAR-2004 (TREMBLrel. 26; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE Tryptophane cysteine-rich surface antigen 72 (Fragment).
DE Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.

```

OX NCBI\_TaxID=5741;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92186850; PubMed=1545800;  
 RA Adam R.D., Yang Y.M., Nash T.E.;  
 RT "The cysteine-rich protein gene family of *Giardia lamblia*: loss of the  
 RT CRP170 gene in an antigenic variant."  
 RL Mol. Cell. Biol. 12:1194-1201(1992).  
 DR PIR: C42125; C42125.  
 DR InterPro: IPR006058; 2Fe2S fd BS.  
 DR InterPro: IPR005127; Giardia\_VSP.  
 DR Pfam: PF03302; VSP; 2.  
 DR PROSITE: PS00197; 2Fe2S\_FERREDOXIN; UNKNOWN\_1.  
 FT NON\_TER 1 677  
 FT TER 677  
 SQ SEQUENCE 677 AA; 68410 MW; E6E621818C0271F5 CRC64;  
  
 Query Match 16.7%; Score 93; DB 2; Length 677;  
 Best Local Similarity 28.4%; Pred. No. 0.8;  
 Matches 25; Conservative 9; Mismatches 36; Indels 18; Gaps 4;

OY 6 EANGNQP---FAANNAARGICVPCQINRVGSVTNAGDLATLTATQ-CTTCCPTGTALDDGV 61  
 DB 304 EANKGTGCKTCKKXGAKPTCSBC---LDGYNSGNGGTIVCEAGANCATCTQAGND- 358  
 OY 62 TDVFDASAQCVCCKPNFYNGSGPQGE 89  
 DB 359 -----KCTKCKRGPFMKNGPTGE 377

## RESULT 9

O9GPP2 TETTH  
 ID O9GPP2\_TETTH PRELIMINARY; PRT; 305 AA.  
 AC O9GPP2\_  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Immobilization antigen LC (Fragment).  
 GN Name=SerLC;  
 OS Tetrahymena thermophila.  
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
 OC Tetrahymenina; Tetrahymenidae; Tetrahymena.  
 OX NCBI\_TaxID=5911;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B;  
 RX MEDLINE=20549003; PubMed=11095959; DOI=10.1006/birc.2000.3857;  
 RA Doerder F.P., Gerber C.A.;  
 RT "Molecular characterization of the SerL paralogs of *Tetrahymena*  
 RT thermophila."  
 RL Biochem. Biophys. Res. Commun. 278:621-626(2000).  
 DR EMBL: AF312772; AAC38118.1; -; mRNA.  
 FT NON\_TER 305  
 FT TER 305  
 SQ SEQUENCE 305 AA; 28863 MW; 0566C353A0253564 CRC64;

Query Match 15.9%; Score 88.5; DB 2; Length 305;  
 Best Local Similarity 35.5%; Pred. No. 1;  
 Matches 38; Conservative 10; Mismatches 36; Indels 23; Gaps 8;

OY 10 NOPFAANNAARGICVPCQINRVGSVTNAGDLATLTATQCTTCCPTGTALDDGVTVF--- 65  
 DB 190 NSSLKADNSA---CV-CKANFYGT-PNA--VAGGATGC-TACPTGTTSTAGTTVIGSCAC 241  
 OY 66 -DRSAA-----QCVCKPNFY-----YNGSGPQGEAPGVQVFAAGAA 101  
 DB 242 PDTNALNSATPVPVCCQKANFYGTPTASGASGCTACPSGQTAPAGSA 288

RESULT 10  
 O9GPP3 TETTH  
 ID O9GPP3\_TETTH PRELIMINARY; PRT; 316 AA.  
 AC O9GPP3\_  
 DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Immobilization antigen LB.  
 GN Name=SerLB;  
 OS Tetrahymena thermophila.  
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
 OC Tetrahymenina; Tetrahymenidae; Tetrahymena.  
 OX NCBI\_TaxID=5911;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B;  
 RX MEDLINE=20549003; PubMed=11095959; DOI=10.1006/birc.2000.3857;  
 RA Doerder F.P., Gerber C.A.;  
 RT "Molecular characterization of the SerL paralogs of *Tetrahymena*  
 RT thermophila."  
 RL Biochem. Biophys. Res. Commun. 278:621-626(2000).  
 DR EMBL: AF312772; AAC38117.1; -; mRNA.  
 FT NON\_TER 316  
 FT TER 316  
 SQ SEQUENCE 316 AA; 30008 MW; 135A0B7D0797A3BD CRC64;

Query Match 15.9%; Score 88.5; DB 2; Length 316;  
 Best Local Similarity 35.5%; Pred. No. 1;  
 Matches 38; Conservative 10; Mismatches 36; Indels 23; Gaps 8;

OY 10 NOPFAANNAARGICVPCQINRVGSVTNAGDLATLTATQCTTCCPTGTALDDGVTVF--- 65  
 DB 190 NSSLKADNSA---CV-CKANFYGT-PNA--VAGGATGC-TACPTGTTSTAGTTVIGSCAC 241  
 OY 66 -DRSAA-----QCVCKPNFY-----YNGSGPQGEAPGVQVFAAGAA 101  
 DB 242 PDTNALNSATPVPVCCQKANFYGTPTASGASGCTACPSGQTAPAGSA 288

## RESULT 11

O7OTU1 GIALA PRELIMINARY; PRT; 724 AA.  
 ID O7OTU1\_GIALA  
 AC O7OTU1\_  
 DT 01-MAR-2004 (Tremblrel. 26, Created)  
 DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE GLP 191\_3328 5502.  
 GN Giardia lamblia ATCC 50803.  
 OS Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiae; Giardia.  
 OX NCBI\_TaxID=184922;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the *Giardia lamblia* genome."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AACB01000101; EAA38433.1; -; Genomic\_DNA.  
 DR HSP: O14763; 1D0G.  
 DR InterPro: IPR005127; Giardia\_VSP.  
 DR Pfam: PF03302; VSP; 1.  
 SQ SEQUENCE 724 AA; 74382 MW; F689C8BFCA051E3 CRC64;

Query Match 15.6%; Score 87; DB 2; Length 724;  
 Best Local Similarity 25.6%; Pred. No. 3.5;  
 Matches 31; Conservative 13; Mismatches 39; Indels 38; Gaps 6;

OY 3 AGCE-ANGNQPAANNAARGICVPCQINRVGSVT-----NAGDLAT 42  
 DB 297 AEGECASGNTHTLEQSPK--ACVPCGDAKNGGILCCSTCSSKTTCTCKCIDGYNSGNGGT 354  
 OY 43 L-ATGCGTCCPTGTALDDGVTVFDRSAAQCVCCKPNFYNGSGPQGEAPGVQVFAAGAA 101  
 DB 355 VTCTACGANCATCSAAGND-----QCTKCKRGPFMKNGPTGSAAGK-----FACDSK 399  
 OY 102 A 102



QY 74 KCKPNFYNGSPQGEAPGVQVFAAGAAA 102  
 DB 202 -CKANFY---GTNNVAVAG---ATGCTA 222

RESULT 15  
 ID 07Q5X6\_GIALA PRELIMINARY; PRT; 536 AA.  
 AC 07Q5X6;  
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE GLP\_44\_3458\_1848.  
 OS Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=184922;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AACB01000113; EAA38112.1; -; Genomic\_DNA.  
 DR InterPro: IPR011641; GCC2\_GCC3.  
 DR Pfam: PF07699; GCC2\_GCC3\_1.  
 SQ SEQUENCE 536 AA; 58170 MW; F72DB5558B3E0C65 CRC64;

Query Match 15.2%; Score 85; DB 2; Length 536;  
 Best Local Similarity 31.3%; Pred. No. 4.1;  
 Matches 26; Conservative 8; Mismatches 37; Indels 12; Gaps 4;  
 QY 23 CVPCCQINRVGSVTNAGDLATLTCSTQCPTGTALDDGVTVFDRSAACQCKKPNFYNN 82  
 DB 419 CVPCCPNNK---TTVHDGALREYC--ECAPGFVLRLD-----DNIDAGCICQCORNSYSK 467  
 QY 83 GG-SPOGEAPGVQVFAAGAAAAG 104  
 DB 468 GGTSTCQCQCPGSGNRMPPTGKSGVG 490

Search completed: December 5, 2005, 06:16:19  
 Job time : 235 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 5, 2005, 05:59:29 ; Search time 46 Seconds

(without alignments)  
188.716 Million cell updates/sec

Title: US-09-196-161d-1

Sequence: 1 GAAQGEANGQPPAANNAAR.....PGGEAPGVVFAAGAAAGV 105

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptcdatc/1/1aa/5.COMB.pep.\*  
2: /cgn2\_6/ptcdatc/1/1aa/6.COMB.pep.\*  
3: /cgn2\_6/ptcdatc/1/1aa/H.COMB.pep.\*  
4: /cgn2\_6/ptcdatc/1/1aa/PCITUS.COMB.pep.\*  
5: /cgn2\_6/ptcdatc/1/1aa/RE.COMB.pep.\*  
6: /cgn2\_6/ptcdatc/1/1aa/backfill1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	100.0	442	2	US-09-498-612-5
2	221	39.6	468	2	US-09-498-612-6
3	84	15.1	613	2	US-09-026-001A-10
4	84	15.1	613	2	US-09-996-620-10
5	84	15.1	621	2	US-09-026-001A-18
6	84	15.1	621	2	US-09-996-620-18
7	83	14.9	1190	2	US-10-053-662A-2
8	78.5	14.1	605	2	US-09-976-594-616
9	78	14.0	3635	2	US-09-845-583A-2
10	78	14.0	3635	2	US-10-037-417-47
11	78	14.0	3635	2	US-10-037-182-4
12	77.5	13.9	862	2	US-09-252-991A-28455
13	77.5	13.9	3647	2	US-09-949-016-10932
14	77	13.8	314	1	US-08-460-309-19
15	77	13.8	314	1	US-08-125-077-19
16	77	13.8	424	1	US-08-419-414-2
17	77	13.8	1551	2	US-09-949-016-6785
18	77	13.8	3712	2	US-10-037-417-48
19	77	13.8	3712	2	US-10-037-417-51
20	76	13.6	1694	2	US-09-560-385A-12
21	76	13.6	1725	2	US-09-560-385A-10
22	75.5	13.5	2508	2	US-09-627-650B-7
23	75.5	13.5	2508	2	US-09-436-063C-7
24	75.5	13.5	2544	2	US-09-627-650B-3
25	75.5	13.5	2544	2	US-09-436-063C-3
26	75.5	13.5	2601	2	US-09-627-650B-9
27	75.5	13.5	2601	2	US-09-436-063C-9

28	75	13.4	169	1	US-08-460-309-20	Sequence 20, Appl
29	75	13.4	169	1	US-08-125-077-20	Sequence 20, Appl
30	75	13.4	1111	1	US-08-317-450B-15	Sequence 15, Appl
31	75	13.4	1111	2	US-08-800-593-15	Sequence 15, Appl
32	75	13.4	1111	2	US-09-756-071B-15	Sequence 15, Appl
33	75	13.4	1172	2	US-09-560-385A-28	Sequence 28, Appl
34	75	13.4	1172	2	US-09-560-385A-32	Sequence 32, Appl
35	75	13.4	1193	2	US-08-117-450B-13	Sequence 13, Appl
36	75	13.4	1193	2	US-08-800-593-13	Sequence 13, Appl
37	75	13.4	1193	2	US-09-560-385A-26	Sequence 26, Appl
38	75	13.4	1193	2	US-09-560-385A-30	Sequence 30, Appl
39	75	13.4	1193	2	US-10-053-662A-31	Sequence 31, Appl
40	75	13.4	1193	2	US-09-756-071B-13	Sequence 13, Appl
41	74	13.3	1461	2	US-10-142-231-86	Sequence 86, Appl
42	72.5	13.0	530	2	US-09-949-016-10781	Sequence 10781, A
43	72.5	13.0	735	2	US-09-999-833A-74	Sequence 74, Appl
44	72.5	13.0	735	2	US-10-020-445A-74	Sequence 74, Appl
45	72.5	13.0	909	2	US-09-949-016-6370	Sequence 6370, Ap

## ALIGNMENTS

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RESULT 1
US-09-498-612-5
; Sequence 5, Application US/09498612
; Patent No. 6846481
; GENERAL INFORMATION:
; APPLICANT: GAERTIG, Jack
; APPLICANT: DICKERSON Jr., Harry W.
; APPLICANT: CLARK, Theodore G.
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
; FILE OF INVENTION: PROTOZA
; FILE REFERENCE: 235.00100101
; CURRENT APPLICATION NUMBER: US/09/498,612
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,634
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/122,372
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,905
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 60/131,121
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: PCT/US00/02966
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Ichthyophthirius multifiliis
US-09-498-612-5

Query Match      100.0%; Score 558; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.7e-52;
Matches 105; Complement 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAQGEANGQPPAANNAARGICVPCQINRVGSVTNAGDATTATQSCPTGTALDDG 60
      |||
Db      56 GAAQGEANGQPPAANNAARGICVPCQINRVGSVTNAGDATTATQSCPTGTALDDG 115
      |||

QY      61 VTDVFDRAAQCVCCKENFYNGSGPGGEAPGVVFAAGAAAGV 105
      |||
Db      116 VTDVFDRAAQCVCCKENFYNGSGPGGEAPGVVFAAGAAAGV 160
      |||

--RESULT 2
US-09-498-612-6
; Sequence 6, Application US/09498612
; Patent No. 6846481
; GENERAL INFORMATION:
```

```

1  APPLICANT: GAERTIG, Jacek
2  APPLICANT: DICKERSON Jr., Harry W.
3  APPLICANT: CLARK, Theodore G.
4  APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
5  TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
6  TITLE OF INVENTION: PROTOZOA
7  FILE REFERENCE: 235.00100101
8  CURRENT APPLICATION NUMBER: US/09/498,612
9  CURRENT FILING DATE: 2000-02-04
10 PRIOR APPLICATION NUMBER: 60/118,634
11 PRIOR FILING DATE: 1999-02-04
12 PRIOR APPLICATION NUMBER: 60/122,372
13 PRIOR FILING DATE: 1999-03-02
14 PRIOR APPLICATION NUMBER: 60/124,905
15 PRIOR FILING DATE: 1999-03-17
16 PRIOR APPLICATION NUMBER: 60/131,121
17 PRIOR FILING DATE: 1999-04-27
18 PRIOR APPLICATION NUMBER: PCT/US00/02966
19 PRIOR FILING DATE: 2000-02-04
20 NUMBER OF SEQ ID NOS: 14
21 SOFTWARE: PatentIn Ver. 2.0
22 SEQ ID NO 6
23 LENGTH: 468
24 TYPE: PRT
25 ORGANISM: Ichthyophthirius multifiliis
26 IS-09-498-612-6

```

Query Match	39.6%	Score 221;	DB 2;	Length 468;
Best Local Similarity	53.3%;	Pred. No. 1e-15;		
Matches 40;	Conservative 8;	Mismatches 25;	Indels 2;	Gaps 1

QY	17	NAARGICVPCQINRVGSVTNAGDLATLATOCSTGCEPTGTILDDGVTYDVFBRSAACQVKCK	76
DB	131	NAGASTCTACPVNRGALTAGNATTIVACNCNVAPEPTGTILDDGVTYDVFBRSAACQVKCK	190

```

QY      77 PNFYNGGSPQGEAP 91
          ||||| : |
Db      191 LNFYNGNN--GNTP 203

```

RESULT 3  
US-09-026-001A-10  
: Sequence 10. Application US/09026001A

GENERAL INFORMATION:  
APPLICANT: Boodhoo, Amechand  
APPLICANT: Seehra, Jasbir

APPLICANT: Sako, Dianne  
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF

ADDRESS: Genetics Institute, Inc.  
87 Cambridgepark Drive  
Cambridge, MA 02142

STATE: Massachusetts  
COUNTRY: USA  
ZTD: 00140

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/MS
```

```

; SOFTWARE: PATENCIN Release #1.0, Version #1.23
;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
;

```

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.

TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: G15293H  
;

```

: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 613 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: JS-09-026-001A-10

```

Query Match	15.1%	Score 84;	DB 2;	Length 613;
Best Local Similarity	29.2%;	Pred. NO. 0.89;		
Matches 28;	Conservative 10;	Mismatches 36;	Indels 22;	Gaps 5.

QY 11 QPAAANNARGIVPCQINRVGSVTNAG---DLATLATQCSITOCPTGTALDDGVTDVDD 66

Db 443 QPAAQCD-SEGCCCKCKFKGAGAGECRAKDDCDLPCLTGTQSAACP-----TDIFQ 492

```

QY      67  RSAAQCYKCKPNFYINGSP-----QGEAPQYV  95
      1 :   |   |   |   |   |   |   |   |
Db      493  RNGTPC-ONNEGVCYNGKCPIMTNOCIALRGPGYKV  527

```

RESULT 4  
US-09-996-620-10

```

; Patent No. 6881404
;
; GENERAL INFORMATION:
;
; APPLICANT: Boodhoo, Amechand

```

Shaw, Gray  
Sako, Dianne  
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM

```

; THERAPEUTIC USES THEREOF
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
;

```

STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts

```

; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
;

```

```

;
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0,  Version #1.25
;
;      CURRENT APPLICATION DATA:
;

```

PRIOR APPLICATION DATA:  
CLASSIFICATION: <Unknown>  
FILING DATE: 27-No. 6881404-2001

FILING DATE: 18-FEB-19  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWN, Scott A.

REFERENCE/DOCKET NUMBER: G15293BE  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224

INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 613 amino acids

ALL: amino acid  
 ;  
 ;  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 ;  
 ;  
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10  
US-09-996-620-10



```

Query Match 15.1% Score 84; DB 2; Length 613;
Best Local Similarity 29.2% Pred. No. 0.89;
Matches 28; Conservative 10; Mismatches 36; Indels 22; Gaps 5

Qy 11 QPFAANNAARGICVPCQINRVGSVYNA-----DLATLATGCGTCTGTALDDGVTVDFD 66
Db 443 QPHAGCD-SEGCCERCKFKGAGAEBAKADDCDDPELCTGGSABCP-----TDLIFQ 492
Qy 67 RSAACVCKKPNFYNGSP-----QGEAPGVY 95
Db 493 RNLGLPC-QNNEGVCYNGKCPIMTNOCIALRGGVAV 527

RESULT 5
US-09-026-001A-18
Sequence 18, Application US/09026001A
Patent No. 6413760
GENERAL INFORMATION:
APPLICANT: Boodhoo, Amechand
APPLICANT: Seenra, Jaadilr
APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026.001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 621 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-026-001A-18

Query Match 15.1% Score 84; DB 2; Length 621;
Best Local Similarity 29.2% Pred. No. 0.91;
Matches 28; Conservative 10; Mismatches 36; Indels 22; Gaps 5

Qy 11 QPFAANNAARGICVPCQINRVGSVYNA-----DLATLATGCGTCTGTALDDGVTVDFD 66
Db 451 QPHAGCD-SEGCCERCKFKGAGAEBAKADDCDDPELCTGGSABCP-----TDLIFQ 500
Qy 67 RSAACVCKKPNFYNGSP-----QGEAPGVY 95
Db 501 RNLGLPC-QNNEGVCYNGKCPIMTNOCIALRGGVAV 535

RESULT 6
US-09-996-620-18
Sequence 18, Application US/09996620

```

```

: Patent No. 6881404
: GENERAL INFORMATION:
: APPLICANT: Boonhoo, Amechand
:           Seehra, Jaabir
:           Shaw, Gray
:           Sako, Dianne
: TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
:                       PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND RELATED PROTEAS
:                       THERAPEUTIC USES THEREOF
:
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/996,620
: FILING DATE: 27-NO. 6881404-2001
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/026, 001
: FILING DATE: 18-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: G15293B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
:
: INFORMATION FOR SEQ ID NO: 18:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 621 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 18:
:
: US-09-996-620-18
:
: Query Match          15.1%; Score 84; DB 2; Length 621,
: Best Local Similarity 29.2%; Pred. No. 0.91,
: Matches 28; Conservative 10; Mismatches 36; Indels 22; Gaps 5;
:
: QY      11  QPFAANNARGICVPCQINRVGSVTNAG----DLATLTATGCGTCTGTALDDGVTVDFD 66
:         |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
: Db      451  QPHAGCD-SEGCGCKCFKGAAGACRAKDDCDLPELCTGGGSAECF-----TDIFQ 500
:
: QY      67  RSAACVCKCKPFIYNGGSP-----QGEAPGVY 95
:         |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
: Db      501  RRGGLPC-QNNEGVCYNGKCPIMTNCIALRGVGV 535
:
: RESULT 7
: US-10-053-662A-2
: Sequence 2, Application US/10053662A
: Patent No. 6916618
: GENERAL INFORMATION:
: APPLICANT: Alexandra Charlesworth
: APPLICANT: Palvia Spirito
: APPLICANT: Guertino Meneguzzi
: APPLICANT: John Baird
: APPLICANT: Keith Lindner
: TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
: TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
: TITLE OF INVENTION: BULLOSA
: FILE REFERENCE: p84us4

```

/ CURRENT APPLICATION NUMBER: US/10/053,662A  
/ CURRENT FILING DATE: 2002-01-24  
/ NUMBER OF SEQ ID NOS: 32  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 2  
/ LENGTH: 1190  
/ TYPE: PRF  
/ ORGANISM: Equine  
/ FEATURE:  
/ OTHER INFORMATION:  
US-10-053-662A-2

Query Match 14.9%; Score 83; DB 2; Length 1190;  
Best Local Similarity 24.4%; Pred. No. 2.5;  
Matches 31; Conservative 16; Mismatches 28; Indels 52; Gaps 7;

QY 20 RQICVPCQINRVGS-----VTNAG---DLATLAT 45  
DB 78 RDRCLPCNCSXGSLARCDNSGRCSCKPVTGDRCLPGRHTLTDAACAQDRLDLS 137  
QY 46 OC-----STOCPGTAL-DDGVTDVFDPSAAQCVKCKPNFY-NGSGPGEAPGVYF 96  
DB 138 KCDDBAGISGPDSSGRVCCKPAVT-----GERCDRCRPGYHLDGNPQG---CTQCF 188  
QY 97 AAGAAA 103  
DB 189 CYGHSAS 195

RESULT 8  
US-09-976-594-616  
/ Sequence 616, Application US/09976594  
/ Patent No. 6673549

/ GENERAL INFORMATION:  
/ APPLICANT: Furness, Michael  
/ APPLICANT: Buchdinder, Jenny  
/ TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
/ FILE REFERENCE: PA-0041 US  
/ CURRENT APPLICATION NUMBER: US/09/976,594  
/ CURRENT FILING DATE: 2001-10-12  
/ PRIOR APPLICATION NUMBER: 60/240,409  
/ PRIOR FILING DATE: 2000-10-12  
/ NUMBER OF SEQ ID NOS: 1143  
/ SOFTWARE: PERL Program  
/ SEQ ID NO 616  
/ LENGTH: 605  
/ TYPE: PRF  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Incyte ID No. 6673549 1692213CH1  
/ NAME/KEY: unsure  
/ LOCATION: 596  
/ OTHER INFORMATION: unknown or other  
US-09-976-594-616

Query Match 14.1%; Score 78.5; DB 2; Length 605;  
Best Local Similarity 27.9%; Pred. No. 3.4;  
Matches 36; Conservative 3; Mismatches 65; Indels 25; Gaps 3;

QY 1 GAAOGEANGNPFAANNAAGLCVPCQINRVGSVTNAGDLA---TLATQC-----STOC 51  
DB 409 GGTGGAAGAAAGAAATTAATCATGTGAAGACTGAATTAAGTTTATACATTGTTTC 468  
QY 52 PGTALDDVTDVFDPSAAQCVKCKPNFYNGSGPGEAPG-----VOY 95  
DB 469 TTTAAAGGATTTACATATCTTTGAGTGAGTGCAAGCAAAATACAAAATTTTAA 528  
QY 96 PAAGAAAAG 104  
DB 529 AAAAGAAAAG 537

RESULT 9  
US-09-845-583A-2  
/ Sequence 2, Application US/09845583A  
/ Patent No. 6635616  
/ GENERAL INFORMATION:  
/ APPLICANT: Burgess, Robert  
/ APPLICANT: Brunken, William Joseph  
/ APPLICANT: Champilaud, Marie-France  
/ APPLICANT: Hunter, Dale  
/ TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
/ FILE REFERENCE: 10287-056001  
/ CURRENT APPLICATION NUMBER: US/09/845,583A  
/ CURRENT FILING DATE: 2001-04-30  
/ PRIOR APPLICATION NUMBER: US 60/200,863  
/ PRIOR FILING DATE: 2000-05-01  
/ NUMBER OF SEQ ID NOS: 18  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 2  
/ LENGTH: 3635  
/ TYPE: PRF  
/ ORGANISM: Mus musculus  
US-09-845-583A-2

Query Match 14.0%; Score 78; DB 2; Length 3635;  
Best Local Similarity 30.5%; Pred. No. 33;  
Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;

QY 21 GICVPCQINRVGSVTN-----AGDLATLATQC-STOCP-----TGTAADDGYTD 63  
DB 1796 GICVGCQHTEDDQCCRCRPGFVSDFSNPASPVCPCPLAVPSNPNFADGCVLRNGRTQ 1855  
QY 64 VFDR---SAQCVCCKPNFYNN 82  
DB 1856 CLCRPGYAGASCERCAPGRFGN 1877

RESULT 10  
US-10-037-417-47  
/ Sequence 417, Application US/10037417  
/ Patent No. 6903201  
/ GENERAL INFORMATION:  
/ APPLICANT: Kekuda, Ramesh  
/ APPLICANT: Alsobrook II, John P  
/ APPLICANT: Tcherneny, Velizar T  
/ APPLICANT: Liu, Xiaohong  
/ APPLICANT: Spytek, Kimberly A  
/ APPLICANT: Paturajan, Meera  
/ APPLICANT: Grosse, William M  
/ APPLICANT: Lepley, Denise M  
/ APPLICANT: Burgess, Catherine E  
/ APPLICANT: Vernet, Corine A.M.  
/ APPLICANT: Li, Li  
/ APPLICANT: Gorman, Linda  
/ APPLICANT: Edinger, Shlomo R  
/ APPLICANT: Sciore, Paul  
/ APPLICANT: Ellerman, Karen  
/ APPLICANT: Malysankar, Uriel M  
/ APPLICANT: Rothenberg, Mark  
/ APPLICANT: Stone, David J  
/ APPLICANT: Boldog, Ferenc L  
/ APPLICANT: Guo, Xiaojia  
/ APPLICANT: Shenoy, Suresh G  
/ APPLICANT: Anderson, David W  
/ APPLICANT: Padigaru, Muralidhara  
/ APPLICANT: Taupier Jr, Raymond J  
/ APPLICANT: Miller, Charles E  
/ APPLICANT: Eilen, Andrew J  
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
/ FILE REFERENCE: 21402-235  
/ CURRENT APPLICATION NUMBER: US/10/037,417  
/ CURRENT FILING DATE: 2002-09-20  
/ PRIOR APPLICATION NUMBER: 60/260,018  
/ PRIOR FILING DATE: 2001-01-05

```

; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-47

Query Match          14.0%; Score 78; DB 2; Length 3635;
Best Local Similarity 30.5%; Pred. No. 33;
Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;
```

```

QY 21 GICVPCQINRVGSVTN-----AGDLATLATOC-STQCP-----TGTALDDGVT 63
DB 1796 GICVGCQHNTEGDCERCRCRPFVSSDBSPASPCVSCPLAVPSNNFADGCVLRNGRTQ 1855
QY 64 VFDR---SAAQCVKCKPNFYNN 82
DB 1856 CLCRPGYAGASCERCAPGFEN 1877
```

```

RESULT 11
US-10-037-182-4
; Sequence 4, Application US/10037182
; Patent No. 6933273
; GENERAL INFORMATION:
; APPLICANT: Trygsvason, Karl
; APPLICANT: Doi, Masayuki
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-182-4
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```

Query Match          14.0%; Score 78; DB 2; Length 3635;
Best Local Similarity 30.5%; Pred. No. 33;
Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;

QY 21 GICVPCQINRVGSVTN-----AGDLATLATOC-STQCP-----TGTALDDGVT 63
DB 1796 GICVGCQHNTEGDCERCRCRPFVSSDBSPASPCVSCPLAVPSNNFADGCVLRNGRTQ 1855
QY 64 VFDR---SAAQCVKCKPNFYNN 82
DB 1856 CLCRPGYAGASCERCAPGFEN 1877
```

```

RESULT 12
US-09-252-991A-28455
; Sequence 28455, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28455
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28455
```

```

Query Match          13.9%; Score 77.5; DB 2; Length 862;
Best Local Similarity 26.3%; Pred. No. 6.8;
Matches 20; Conservative 11; Mismatches 18; Indels 27; Gaps 3;
```

```

QY 2 AAGGANGNPPFANNNARGI--CVPQINRVGSVTNAGDLATLATATOCSTQCP-----TGTALDDGVT 59
DB 639 AARGESRARKKSGSDRAQGLGDCIDCQ-----QCVQVCPGTGIDIRD 680
QY 60 GVTDFVDRSAQCVKC 75
DB 681 GL-----QIACIGC 689
```

```

RESULT 13
US-09-949-016-10932
; Sequence 10932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10932
; LENGTH: 3647
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10932
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```

Query Match          13.9%; Score 77.5; DB 2; Length 3647;
Best Local Similarity 27.7%; Pred. No. 38;
Matches 23; Conservative 9; Mismatches 28; Indels 23; Gaps 4;

QY 21 GICVPCQIN-----RVGSVTNAGDLATLATATOCSTQCP-----TGTALDDGVT 62
DB 1812 GVCVDCQHNTEGAGHCERCQAGFVSSRDPSTPCVSC--PPLVPSNNFADGCVLRNGRT 1869
QY 63 DVFDR---SAAQCVKCKPNFYNN 82
DB 1870 QCLCKPGYAGASCERCAPGFEN 1892
```

RESULT 14  
US-08-460-309-19  
Sequence 19, Application US/08460309  
Patent No. 5837496  
GENERAL INFORMATION:  
APPLICANT: Engvall, Eva  
APPLICANT: Leivo, Ilmo  
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
TITLE OF INVENTION: Fragments and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,309  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,077  
FILING DATE: 22-SEP-1993  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 314 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-460-309-19  
Query Match 13.8%; Score 77; DB 1; Length 314;  
Best Local Similarity 23.9%; Pred. No. 2.3;  
Matches 21; Conservative 17; Mismatches 20; Indels 30; Gaps 5;  
QY 23 CVPQINRVGSVTNAGDLATLATQGST-----QC-----PTGTALD---DGV-TD 63  
DB 220 CKAECNKGITNDNCVTTGECCKCLTNFGDNCRCRKHGYNPTCSYCDNDNGTSE 279  
QY 64 VFDRSAQCV-----KCKPNFY 80  
DB 280 ICKKSGQCICREGFGPRDQCLPFGY 307  
RESULT 15  
US-08-125-077-19  
Sequence 19, Application US/08125077  
Patent No. 5872231  
Patent No. 5872231 5840863  
GENERAL INFORMATION:  
APPLICANT: Engvall, Eva  
APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
TITLE OF INVENTION: Fragments and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,077  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 314 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-125-077-19  
Query Match 13.8%; Score 77; DB 1; Length 314;  
Best Local Similarity 23.9%; Pred. No. 2.3;  
Matches 21; Conservative 17; Mismatches 20; Indels 30; Gaps 5;  
QY 23 CVPQINRVGSVTNAGDLATLATQGST-----QC-----PTGTALD---DGV-TD 63  
DB 220 CKAECNKGITNDNCVTTGECCKCLTNFGDNCRCRKHGYNPTCSYCDNDNGTSE 279  
QY 64 VFDRSAQCV-----KCKPNFY 80  
DB 280 ICKKSGQCICREGFGPRDQCLPFGY 307  
Search completed: December 5, 2005, 06:17:09  
Job time : 47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 5, 2005, 06:12:28 ; Search time 165 Seconds  
(Without alignments)  
265,891 Million cell updates/sec

Title: US-09-196-161d-1

Sequence: 1 GAAOGEANGQPPFANNAAAR.....POGEAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	100.0	442	5	US-10-878-694-5 Sequence 5, Appli
2	221	39.6	468	5	US-10-878-694-6 Sequence 6, Appli
3	87.5	15.7	3265	4	US-10-184-644-257 Sequence 257, App
4	87.5	15.7	3265	4	US-10-184-634-257 Sequence 257, App
5	87.5	15.7	3265	4	US-10-063-685-69 Sequence 69, Appl
6	85.5	15.3	914	3	US-09-975-143-47 Sequence 47, Appl
7	85.5	15.3	1076	4	US-10-028-072-219 Sequence 219, App
8	85.5	15.3	1076	4	US-10-140-808-219 Sequence 219, App
9	85.5	15.3	1076	4	US-10-121-049-219 Sequence 219, App
10	85.5	15.3	1076	4	US-10-123-904-219 Sequence 219, App
11	85.5	15.3	1076	4	US-10-140-470-219 Sequence 219, App
12	85.5	15.3	1076	4	US-10-175-746-219 Sequence 219, App
13	85.5	15.3	1076	4	US-10-176-918-219 Sequence 219, App
14	85.5	15.3	1076	4	US-10-176-921-219 Sequence 219, App
15	85.5	15.3	1076	4	US-10-137-865-219 Sequence 219, App
16	85.5	15.3	1076	4	US-10-140-474-219 Sequence 219, App
17	85.5	15.3	1076	4	US-10-143-431-219 Sequence 219, App
18	85.5	15.3	1076	4	US-10-143-114-219 Sequence 219, App
19	85.5	15.3	1076	4	US-10-143-419-219 Sequence 219, App
20	85.5	15.3	1076	4	US-10-123-262-219 Sequence 219, App
21	85.5	15.3	1076	4	US-10-143-423-219 Sequence 219, App
22	85.5	15.3	1076	4	US-10-121-050-219 Sequence 219, App
23	85.5	15.3	1076	4	US-10-141-755-219 Sequence 219, App
24	85.5	15.3	1076	4	US-10-143-032-219 Sequence 219, App
25	85.5	15.3	1076	4	US-10-123-108-219 Sequence 219, App
26	85.5	15.3	1076	4	US-10-123-236-219 Sequence 219, App
27	85.5	15.3	1076	4	US-10-123-261-219 Sequence 219, App

28	85.5	15.3	1076	4	US-10-140-921-219 Sequence 219, App
29	85.5	15.3	1076	4	US-10-140-928-219 Sequence 219, App
30	85.5	15.3	1076	4	US-10-121-045-219 Sequence 219, App
31	85.5	15.3	1076	4	US-10-123-292-219 Sequence 219, App
32	85.5	15.3	1076	4	US-10-123-903-219 Sequence 219, App
33	85.5	15.3	1076	4	US-10-124-819-219 Sequence 219, App
34	85.5	15.3	1076	4	US-10-124-822-219 Sequence 219, App
35	85.5	15.3	1076	4	US-10-140-925-219 Sequence 219, App
36	85.5	15.3	1076	4	US-10-160-498-219 Sequence 219, App
37	85.5	15.3	1076	4	US-10-124-824-219 Sequence 219, App
38	85.5	15.3	1076	4	US-10-127-825A-219 Sequence 219, App
39	85.5	15.3	1076	4	US-10-127-829A-219 Sequence 219, App
40	85.5	15.3	1076	4	US-10-127-835A-219 Sequence 219, App
41	85.5	15.3	1076	4	US-10-127-839A-219 Sequence 219, App
42	85.5	15.3	1076	4	US-10-127-901A-219 Sequence 219, App
43	85.5	15.3	1076	4	US-10-128-693A-219 Sequence 219, App
44	85.5	15.3	1076	4	US-10-131-813A-219 Sequence 219, App
45	85.5	15.3	1076	4	US-10-131-818A-219 Sequence 219, App

## ALIGNMENTS

```
RESULT 1
US-10-878-694-5
; Sequence 5, Application US/10878694
; Publication No. US20050106164A1
; GENERAL INFORMATION:
; APPLICANT: GAERTIG, Jacek
; APPLICANT: DICKERSON Jr., Harry W.
; APPLICANT: CLARK, Theodore G.
; TITLE OR INVENTION: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
; TITLE OR INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
; FILE REFERENCE: 235, 00100101
; CURRENT APPLICATION NUMBER: US/10/878,694
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: US/09/498,612
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,634
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/122,372
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,905
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 60/131,121
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: PCT/US00/02966
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Ichthyophthirius multifiliis
US-10-878-694-5
Query Match      100.0%; Score 558; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.7e-50;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy      1 GAAOGEANGQPPFANNAAAGICVPCQINRVGSVTNAGDLATLATOCSCTGCTALDDG 60
Db      56 GAAOGEANGQPPFANNAAAGICVPCQINRVGSVTNAGDLATLATOCSCTGCTALDDG 115
Cy      61 VTDFDRSAACVCKENFYNGSGSPOGEAPGVVFAAGAAAGV 105
Db      116 VTDFDRSAACVCKENFYNGSGSPOGEAPGVVFAAGAAAGV 160
RESULT 2
US-10-878-694-6
; Sequence 6, Application US/10878694
```

```

1 Publication No. US20050106164A1
2 GENERAL INFORMATION:
3 APPLICANT: GAERTIG, Jaecq
4 APPLICANT: DICKERSON Jr., Harry W.
5 APPLICANT: CLARK, Theodore G.
6 APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
7 TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
8 TITLE OF INVENTION: PROTOZOA
9 FILE REFERENCE: 235,00100101
10 CURRENT APPLICATION NUMBER: US/10/878,694
11 CURRENT FILING DATE: 2004-06-28
12 PRIOR APPLICATION NUMBER: US/09/498,612
13 PRIOR FILING DATE: 2000-02-04
14 PRIOR APPLICATION NUMBER: 60/118,634
15 PRIOR FILING DATE: 1999-02-04
16 PRIOR APPLICATION NUMBER: 60/122,372
17 PRIOR FILING DATE: 1999-03-02
18 PRIOR APPLICATION NUMBER: 60/124,905
19 PRIOR FILING DATE: 1999-03-17
20 PRIOR APPLICATION NUMBER: 60/131,121
21 PRIOR FILING DATE: 1999-04-27
22 PRIOR APPLICATION NUMBER: PCT/US00/02966
23 PRIOR FILING DATE: 2000-02-04
24 NUMBER OF SEQ ID NOS: 14
25 SOFTWARE: PatentIn Ver. 2.0
26
27 SEQ ID NO 6
28 LENGTH: 468
29 TYPE: PRT
30 ORGANISM: Ichthyophthirius multifiliis
31 US-10-878-694-6

```

	Query Match	Similarity	Score	DB	Length	468;
Best Local	53.3%	39.6%	22;	DB	5;	
Matches	40;	Conservative	8;	Mismatches	25;	Indels 2; Gaps 1
QY	17	NAARICVPCQINRRGSGVTNAGDLATLTATGCGTQCTGTALDDGVDVDFSRALAOQVCKK	76			
Db	131	NAGASTCTACPCPNRRGALTAGNAATIVACQVACGTALDDGVTDDYRSTECVKCR	190			
QY	77	ENFYNYGSGPQGEAP	91			
Db	191	LNFFNYNGNN--GNTP	203			

```

RESULT 3
US-10-184-644-257
: Sequence 257, Application US/10184644
: Publication No. US20030044930A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C227
: CURRENT APPLICATION NUMBER: US/10/184,644
: CURRENT FILING DATE: 2002-06-28
: NUMBER OF APPLICATION removed - See file wrapper or Palm
: SEQ ID NO 257
: SEQ ID NO NOS: 612
: LENGTH: 3265
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-184-644-257

```

	Query Match	15.7%	Score 87.5;	DB 4;	length 3265;
	Best Local Similarity	33.0%;	Pred. No. 9.7;		
	Matches	30;	Mismatches	48;	Gaps 4;
Oy	14 AANNAARGICVPCQINRVGSVTNAGDIATATGCGTCSTCPTGTALDDGV-TDVFDRSAQC	72			
	:				
Dd	3123 AATTAAATATATC---TATCTGA GTAGTGCAA-AATCAAGTAAGAGACCAATAAACC	3177			
Oy	73 VKCKENFYNGSGSFOGEAPGVGFPAAGAAA	103			
Dd	3178 AACATT---TGGAAAAAAAAAAAAAAAAAAAAA	3205			

```

RESULT 4
US-10-184-634-257
Sequence 257, Application US/10184634
Publication No. US2003068684A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 257
LENGTH: 3265
TYPE: DNA
ORGANISM: Homo Sapien
US-10-184-634-257

```

```

Query Match          15.7%; Score 87.5; DB 4; Length 3265;
Best Local Similarity 33.0%; Pred. No. 9.7;
Matches 30; Conservative 4; Mismatches 48; Indels 9; Gaps 4;

QY      14 AANNAAAGICVPCQINVEGVTNAGDIATATQCSCTCPTGTALDDGV-TDVPDSAAQC 72
Db       3123 AATTAATAATCATC-----TATCTAGTAGTGTCAA-AATACAGTAAAGAGACCAATAATAAC 3177
QY      73 VKCKENFYNGGSPQGEAPGVQVFAAGAAA 103
Db       3178 AACATT--TGAAAAAAAAAAAAAAAAAA 3205

RESULT 5
US-10-063-685-69
: Sequence 69, Application US/10063685
: Publication No. US20030180909A1
: GENERAL INFORMATION:
: APPLICANT: Eaton, Dan L.
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P933ORIC1
: CURRENT APPLICATION NUMBER: US/10/063.685

```







```
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria A.
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 219
LENGTH: 1076
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-808-219
```

```
Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY 1 GAAQGEANGNPFAANNAAGICVPCQINRVGSVTNAGDLATLATOCSTOCPG-----TA 56
DB 469 GAAACAAAGAAATCTACAAAGCCATCA--GTGAACGTGATATTTCTTCTTCCTGGATTAA 526
```

```
QY 57 LDDGVTDVFDPSAAQCCKPKNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGTGAAAGC-----AGTCAGTAAAC-CAAGCCAAAG 563
```

RESULT 9  
US-10-121-049-219

Sequence 219, Application US/10121049  
Publication No. US2003022239A1

GENERAL INFORMATION:

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerltsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 219
LENGTH: 1076
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-219
```

```
Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY 1 GAAQGEANGNPFAANNAAGICVPCQINRVGSVTNAGDLATLATOCSTOCPG-----TA 56
DB 469 GAAACAAAGAAATCTACAAAGCCATCA--GTGAACGTGATATTTCTTCTTCCTGGATTAA 526
```

```
QY 57 LDDGVTDVFDPSAAQCCKPKNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGTGAAAGC-----AGTCAGTAAAC-CAAGCCAAAG 563
```

RESULT 10

US-10-123-904-219

Sequence 219, Application US/10123904  
Publication No. US2003022238A1

GENERAL INFORMATION:

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerltsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 219
LENGTH: 1076
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-219
```

```
Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY 1 GAAQGEANGNPFAANNAAGICVPCQINRVGSVTNAGDLATLATOCSTOCPG-----TA 56
DB 469 GAAACAAAGAAATCTACAAAGCCATCA--GTGAACGTGATATTTCTTCTTCCTGGATTAA 526
```

```
QY 57 LDDGVTDVFDPSAAQCCKPKNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGTGAAAGC-----AGTCAGTAAAC-CAAGCCAAAG 563
```

RESULT 11

US-10-140-470-219

Sequence 219, Application US/10140470  
Publication No. US2003022231A1

GENERAL INFORMATION:

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerltsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
```

```
/ APPLICANT: Smith,Victoria
/ APPLICANT: Stewart,Timothy A.
/ APPLICANT: Tumas,Daniel
/ APPLICANT: Matanabe,Colin K
/ APPLICANT: Wood,William
/ APPLICANT: Zhang,Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C160
/ CURRENT APPLICATION NUMBER: US/10/140,470
/ CURRENT FILING DATE: 2002-05-06
/ Prior Application removed - See Palm or File Wrapper
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-140-470-219
```

```
Query Match          15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY      1  GAAAGEANGNPFANNARAGICVPCQINRVSVTNAGDLATLATQCSTQCPTG----TA 56
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      469  GAAACAAAGGAATCTCAAAAGCCATCA--GTGAAGTGAATATTCTTCTTCTGGATTAA 526
```

```
QY      57  LDDGVTVDFDRSAQCVCCKPFYNGSPGSEAPGVGFAGAAAG 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527  AAAATTATTGGAAAGC-----AGTCAGTAAC-CAAAGCCAG 563
```

```
RESULT 12
US-10-175-746-219
/ Sequence 219, Application US/10175746
/ Publication No. US20030027270A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Matanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C353
/ CURRENT APPLICATION NUMBER: US/10/175,746
/ CURRENT FILING DATE: 2002-06-19
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-175-746-219
```

```
Query Match          15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
Db      469  GAAACAAAGGAATCTCAAAAGCCATCA--GTGAAGTGAATATTCTTCTTCTGGATTAA 526
QY      57  LDDGVTVDFDRSAQCVCCKPFYNGSPGSEAPGVGFAGAAAG 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527  AAAATTATTGGAAAGC-----AGTCAGTAAC-CAAAGCCAG 563

RESULT 13
US-10-176-918-219
/ Sequence 219, Application US/10176918
/ Publication No. US20030027275A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Matanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C382
/ CURRENT APPLICATION NUMBER: US/10/176,918
/ CURRENT FILING DATE: 2002-06-20
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-918-219

Query Match          15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6;
Matches 34; Conservative 4; Mismatches 53; Indels 17; Gaps 4;
```

```
QY      1  GAAAGEANGNPFANNARAGICVPCQINRVSVTNAGDLATLATQCSTQCPTG----TA 56
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      469  GAAACAAAGGAATCTCAAAAGCCATCA--GTGAAGTGAATATTCTTCTTCTGGATTAA 526
QY      57  LDDGVTVDFDRSAQCVCCKPFYNGSPGSEAPGVGFAGAAAG 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527  AAAATTATTGGAAAGC-----AGTCAGTAAC-CAAAGCCAG 563

RESULT 14
US-10-176-921-219
/ Sequence 219, Application US/10176921
/ Publication No. US20030027276A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
```

```
/ APPLICANT: Tuma, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C288
/ CURRENT APPLICATION NUMBER: US/10/176,921
/ CURRENT FILING DATE: 2002-06-20
/ Prior Application removed - See file wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-921-219
```

```
Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6; Indels 17; Gaps 4;
Matches 34; Conservative 4; Mismatches 53;
```

```
QY 1 GAAOGEANGNPFAANNAARGICVPCQINRVGSVTNAGDLATLTCGTCGPTG---TA 56
DB 469 GAAACAAAGATCTACAAAGCCATCA--GTGAAGTGAATATCTTCTTCTCGATTA 526
```

```
QY 57 LDDGVTDVFDPSAAQCVKCKPNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGGAAGC-----AGTCAGTAAAC-CAAGCCAAAG 563
```

## RESULT 15

```
US-10-137-865-219
/ Sequence 219, Application US/10137865
/ Publication No. US20030032155A1
```

## GENERAL INFORMATION:

```
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Garltsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tuma, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C154
/ CURRENT APPLICATION NUMBER: US/10/137,865
/ CURRENT FILING DATE: 2002-05-03
/ Prior Application removed - See Palm or File wrapper
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 219
/ LENGTH: 1076
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-137-865-219
```

```
Query Match 15.3%; Score 85.5; DB 4; Length 1076;
Best Local Similarity 31.5%; Pred. No. 4.6; Indels 17; Gaps 4;
Matches 34; Conservative 4; Mismatches 53;
```

```
QY 1 GAAOGEANGNPFAANNAARGICVPCQINRVGSVTNAGDLATLTCGTCGPTG---TA 56
DB 469 GAAACAAAGATCTACAAAGCCATCA--GTGAAGTGAATATCTTCTTCTCGATTA 526
```

```
QY 57 LDDGVTDVFDPSAAQCVKCKPNFYNGSPQGEAPGVQVFAAGAAAG 104
DB 527 AAATATTGGAAGC-----AGTCAGTAAAC-CAAGCCAAAG 563
```

```
Search completed: December 5, 2005, 06:21:06
Job time : 166 secs
```

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A: Experimental source: trophozoites  
 N: Note: sequence extracted from NCBI backbone (NCBITN:88443, NCBIIP:88444); this ORF is not

C/Keywords: surface antigen

Query Match 16.7%; Score 93; DB 2; Length 677;

Best Local Similarity 28.4%; Pred. No. 0.22; Mismatches 36; Indels 18; Gaps 4;

Matches 25; Conservative 9; Mismatches 36; Indels 18; Gaps 4;

QY 6 EANGNP---FAANNAARGICVPCQINRVGSVTNAGDLATLQ-CSTQCPGTALDDGV 61

DB 304 EANKGPCKCTCKGNKAKPTCSSEC---LDGYNSNGGTVCACGANCATCTQAGND- 358

QY 62 TDVFDRAAQCVCCKPFFYNGSSPOGE 89

DB 359 -----CKTKCKGFFMKNGPFG 377

RESULT 3

T00209

MEGF8 protein - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Jul-1999 #sequence\_rev1510n 22-Jan-1999 #text\_change 21-Jul-2000

C/Accession: T00209

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A/Reference number: Z14126; MUID:98360089; PMID:9693030

A/Accession: T00209

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-11737 <NA>

A/Cross-references: UNIPARC:UPI000006FDFP; EMBL:AB011541; NID:G3449307; PIDN:BAA32469.1;

A/Experimental source: brain; clone HG1392

C/Genetics:

A/Gene: MEGF8

A/Map position: 19q12

Query Match 15.1%; Score 84.5; DB 2; Length 1737;

Best Local Similarity 33.8%; Pred. No. 3.6; Mismatches 28; Indels 17; Gaps 3;

Matches 25; Conservative 4; Mismatches 28; Indels 17; Gaps 3;

QY 21 GICVPCQINRVGSVTNAGDLATLQCSNQC-----TGTAADGVTDFDRAAQCVC 74

DB 1267 GKCTKCCCN-----GHADTCNEBDGTGCPQNNTEGTGCGSSPSDRDCKYQCK 1318

QY 75 CKPFFYNGSSPOG 88

DB 1319 CRESFH---GSPFG 1329

RESULT 4

A45664

variant-specific surface protein VSP1267 - Giardia lamblia

C/Species: Giardia lamblia

C/Date: 22-Apr-1993 #sequence\_rev1510n 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: A45664

R:Mowatt, M.R.; Aggarwal, A.; Nash, T.E.

Mol. Biochem. Parasitol. 49, 215-227, 1991

A/Title: Carboxy-terminal sequence conservation among variant-specific surface proteins

A/Reference number: A45664; MUID:9211058; PMID:1175165

A/Accession: A45664

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-596 <MOW>

A/Cross-references: UNIPROT:Q07317; UNIPARC:UPI000016BEE6; GB:M63966; NID:G159140; PID:G

A/Note: sequence extracted from NCBI backbone (NCBIN:77609, NCBI:77610)

Query Match 14.0%; Score 78; DB 2; Length 596;

Best Local Similarity 23.0%; Pred. No. 5.7; Mismatches 36; Indels 48; Gaps 6;

Matches 28; Conservative 10; Mismatches 36; Indels 48; Gaps 6;

QY 43 LATQCSSTQCPGTALDDG-----VTDFDRAAQCVCCKPFFYNG 83

DB 297 LGDACTLCDPAGTAVVSGDSGVCCKPCHNTACGCTD--DRETS-CTACYPGSLYSESN 353

QY 84 GS 85

DB 354 GA 355

RESULT 5

T10053

laminin alpha 5 chain - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 16-Jul-1999 #sequence\_rev1510n 16-Jul-1999 #text\_change 09-Jul-2004

C/Accession: T10053

R:Miner, J.H.; Lewis, R.M.; Sane, J.R.

submitted to the EMBL Data Library, November 1997

A/Reference number: Z16923

A/Accession: T10053

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-3635 <MIN>

A/Cross-references: UNIPROT:Q61001; UNIPARC:UPI000004C5E8; EMBL:U37501; NID:G2599231; PI

F:1888-1939/Domain: laminin-type EGF-like homology <LEG>

F:1942-1970/Domain: EGF homology <EGF>

Query Match 14.0%; Score 78; DB 2; Length 3635;

Best Local Similarity 30.5%; Pred. No. 31; Mismatches 30; Indels 20; Gaps 4;

Matches 25; Conservative 7; Mismatches 30; Indels 20; Gaps 4;

QY 21 GICVPCQINRVGSVTN-----AGDLATLQCSNQC-----TGTAADGVTDF 63

DB 1796 GICVGCQHTBBDQCERCAPEVSSDPSPAPSCVSCCPPLAVPSNNFADGCVLRNGRTQ 1855

QY 64 VFDR---SNAQCVCCKPFFYNG 82

DB 1856 GICRPGYAGASCERCAPGFGN 1877

RESULT 6

D83130

probable iron-sulfur protein PA4131 [imported] - Pseudomonas aeruginosa (strain PAO1)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_rev1510n 15-Sep-2000 #text\_change 09-Jul-2004

C/Accession: D83130

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lam,

., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathc

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: D83130

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-573 <STO>

A/Cross-references: UNIPROT:Q9HW0; UNIPARC:UPI000000C5C28; GB:AE004829; GB:AE004091; NIT

A/Experimental source: strain PAO1

C/Genetics:

A/Gene: PA4131

C/Superfamily: nitrogen fixation protein fixG; ferredoxin 2[Fe-4S] homology

Query Match 13.9%; Score 77.5; DB 2; Length 573;

Best Local Similarity 26.3%; Pred. No. 6.1; Mismatches 18; Indels 27; Gaps 3;

Matches 20; Conservative 11; Mismatches 18; Indels 27; Gaps 3;

QY 2 AAOGEANGQPPAANNAARGI--CVPCQINRVGSVTNAGDLATLQCSSTQCPGTALDD 59

DB 350 AARGSRARRKKGSPRAAGLGDCTDCQ-----QCQVQVPTGIDIND 391

QY 60 GVTDFDRAAQCVCCK 75

Db 392 GL-----QIATGCC 400

RESULT 7  
T25933  
hypothetical protein W02C12.1 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T25933  
R/Murray, J.; Wohlmann, P.  
submitted to the EMBL Data Library, December 1996  
A/Description: The sequence of C. elegans cosmid W02C12.  
A/Reference number: Z20112  
A/Accession: T25933  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1372 <MUR>  
A/Cross-references: UNIPROT:P91526; UNIPARC:UPI000075513; EMBL:U80815; PIDN:AAB37995.1  
A/Experimental source: strain Bristol N2; clone W02C12  
C/Genetics:  
A/Gene: CESP:W02C12.1  
A/Map position: 4  
A/Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 13.8%; Score 77; DB 2; Length 1372;  
Best Local Similarity 21.2%; Pred. No. 16;  
Matches 28; Conservative 14; Mismatches 50; Indels 40; Gaps 5;

QY 3 AAGEANGNOPFAANNARGICVPCQINRVGS-----VTNAGDLATLATQCST 49  
Db 1036 SEDECRDECPDGBQLSAGVCPQIGTYSRGNKNCVACPPTTETATMTSTREQCNT 1095  
QY 50 Q-----CPTGTALDDGVTVDFDRSAQCCKPKNFYNGSGSPGAPG 92  
Db 1096 PKCKPGQFLVETKNGCFCPRGTQN-----EEGSTCKLCPD--HTTAAP-GATAE 1145

QY 93 VQVFPAAGAAAG 104  
Db 1146 SOCFSTNQCATG 1157

RESULT 8  
S18253  
laminin alpha-1 chain precursor - fruit fly (*Drosophila melanogaster*)  
C/Species: *Drosophila melanogaster*  
C/Date: 16-Sep-1992 #sequence\_revision 24-Jul-1997 #text\_change 09-Jul-2004  
C/Accession: S28399; S18253  
R/Kusche-Gullberg, M.; Garrison, K.; Mackrell, A.J.; Fessler, L.I.; Fessler, J.H.  
EMBO J. 11, 4519-4527, 1992  
A/Title: Laminin A chain: expression during *Drosophila* development and genomic sequence.  
A/Reference number: S28399; MUID:93049203; PMID:1425586  
A/Accession: S28399  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-3712 <KUS>  
A/Cross-references: UNIPROT:Q00174; UNIPARC:UPI000004BE1C; GB:M66388; NID:G157799; PIDN:R/Garrison, K.; Mackrell, A.J.; Fessler, J.H.  
J. Biol. Chem. 266, 22899-22904, 1991  
A/Title: *Drosophila* laminin A chain sequence. Inter-species comparison, and domain structure  
A/Reference number: S18253; MUID:92078147; PMID:1744083  
A/Accession: S18253  
A/Molecule type: mRNA  
A/Residues: 1762-3712 <GAR>  
A/Cross-references: UNIPARC:UPI000016BC67; EMBL:M75882; NID:G157797; PIDN:AAA28661.1; P/C/Genetics:  
A/Gene: FLYBase:Lana  
A/Cross-references: FLYBase:FBgn0002526  
C/Suprafamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h  
C/Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular  
F/273-330/Domain: laminin-type EGF-like homology <LEG>  
F/333-400/Domain: laminin-type EGF-like homology <LEG2>  
F/541-584/Domain: laminin-type EGF-like homology <LEG1>

F/1776-2115/Domain: III <DOM3>  
F/1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>  
F/1809-1856/Domain: laminin-type EGF-like homology <LE2>  
F/1859-1914/Domain: laminin-type EGF-like homology <LE3>  
F/1917-1967/Domain: laminin-type EGF-like homology <LE4>  
F/1970-2014/Domain: laminin-type EGF-like homology <LE5>  
F/2017-2061/Domain: laminin-type EGF-like homology <LE6>  
F/2064-2109/Domain: laminin-type EGF-like homology <LE7>  
F/2116-2697/Domain: I/II, heptad repeats <DOM2>  
F/2698-3712/Domain: G <DOMG>  
F/2698-3712/Domain: repeat G1 <RG1>  
F/2864-3048/Domain: repeat G2 <RG2>  
F/3049-3223/Domain: repeat G3 <RG3>  
F/3079-3200/Domain: laminin G repeat homology <LG3>  
F/3334-3528/Domain: repeat G4 <RG4>  
F/3529-3712/Domain: repeat G5 <RG5>  
F/1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,

Query Match 13.8%; Score 77; DB 2; Length 3712;  
Best Local Similarity 23.9%; Pred. No. 40;  
Matches 21; Conservative 17; Mismatches 20; Indels 30; Gaps 5;

QY 23 CVPCQINRVGSVTNAGDLATLATQCST-----QC-----PTGTALD--DGV-TD 63  
Db 492 CKACECNKIGSITNDGCVTTGCECKLTNFGDNCERCKHGYFNYPTCSYCDNCGTESE 551

QY 64 VFDRSAQCV-----KCKNPFY 80  
Db 552 ICKKSGQCTCRGFGGPRCDCLPGFY 579

RESULT 9  
A35502  
major surface-labeled trophozoite antigen precursor - *Giardia lamblia*  
C/Species: *Giardia lamblia*  
C/Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 09-Jul-2004  
C/Accession: A35502  
R/Gillin, F.D.; Hagblom, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So,  
Proc. Natl. Acad. Sci. U.S.A. 87, 4463-4467, 1990  
A/Title: Isolation and expression of the gene for a major surface protein of *Giardia la*  
A/Reference number: A35502; MUID:90280395; PMID:2352929  
A/Accession: A35502  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-713 <GIL>  
A/Cross-references: UNIPROT:P21849; UNIPARC:UPI0000137732; GB:M3641; NID:G159131; PID: C/Keywords: surface antigen; transmembrane protein

Query Match 13.5%; Score 75.5; DB 2; Length 713;  
Best Local Similarity 27.5%; Pred. No. 12;  
Matches 28; Conservative 10; Mismatches 35; Indels 29; Gaps 6;

QY 3 AAGEANGNOPFAANNARGI--CVPCQINRVGSVTNAGDLATLATQC----- 47  
Db 135 ACGDTTGVTIAAGNTYKGIADCAEGCAPATAGAEAGKAT-CTKGVGSKVLKDNVCVD 193

QY 48 STCCPTCT-----ALDDGVTVDFDRSAQCCKPKNFYNGG 84  
Db 194 KAQCSGSGTNRKFAVVD-----SENGNKCVCSDNL--NGG 227

RESULT 10  
A44018  
laminin B2c chain precursor, long form - human  
N/Alternate names: cell-adhesive scatter factor ladsln; laminin 10SK chain; nicein 100K  
C/Species: *Homo sapiens* (man)  
C/Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A44018; B44018; S41097; A49401  
R/Kallunki, P.; Sainio, K.; Bddy, R.; Byers, M.; Kallunki, T.; Sariola, H.; Beck, K.; H  
J. Cell Biol. 119, 679-693, 1992  
A/Title: A truncated laminin chain homologous to the B2 chain: structure, spatial expre  
A/Reference number: A44018; MUID:93016279; PMID:1183240  
A/Accession: A44018

A:Molecule type: mRNA  
A:Residues: 1-1193 <KAL>  
A:Cross-references: UNIPROT:Q13753; UNIPARC:UPI000003490C; GB:215008; NID:g34229; PIDN:C  
A:Experimental source: fibroblastoma HT1080 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:116635)  
A:Accession: B44018  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-1109, 'GM' <KA2>  
A:Cross-references: UNIPARC:UPI000014666C; GB:215009; GB:S47253; NID:g34231; PIDN:CAA787  
A:Experimental source: fibroblastoma HT1080 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:116637)  
R:Valley, J.; Verrando, P.; Chambliaud, M.F.; Gerecke, D.; Wagman, D.W.; Baudoin, C.; Ab  
Eur. J. Biochem. 219, 209-218, 1994  
A:Title: The 100-kDa chain of nicotinylaminin is a laminin B2 chain variant.  
A:Reference number: S41097; MUID:94139694; PMID:8306988  
A:Accession: S41097  
A:Molecule type: mRNA  
A:Residues: 1-11, 'L', 13-472, 'M', 474-520, 'N', 522-856, 'R', 858-1193 <VA1>  
A:Cross-references: UNIPARC:UPI000016ADE1; EMBL:X73902; NID:g452754; PIDN:CAA52108.1; PI  
A:Experimental source: keratinocytes  
R:Hayazaki, K.; Kikawa, Y.; Nakamura, A.; Yasumitsu, H.; Umeda, M.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11767-11771, 1993  
A:Title: A large cell-adhesive scatter factor secreted by human gastric carcinoma cells.  
A:Reference number: A49401; MUID:94089713; PMID:8265624  
A:Accession: A49401  
A:Molecule type: protein  
A:Residues: 435-441, 'X', 443-444, 'X', 446-449 <MT>  
A:Cross-references: UNIPARC:UPI000017C28E  
C:Genetic:  
A:Gene: GDB:LAMC2; EBR2; EBR2A; L; LAMB2T  
A:Cross-references: GDB:136225; OMIM:150292  
A:Map position: 1q31-1q31  
C:Keyword: alternative splicing; basement membrane; extracellular matrix; glycoprotein  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-1193/Product: laminin B2 chain #status predicted <MAT>  
F:84-128/Domain: laminin-type EGF-like homology <LEG>  
F:517-570/Domain: laminin-type EGF-like homology <LEG>  
Query Match 13.4%; Score 75; DB 2; Length 1193;  
Best Local Similarity 26.7%; Pred. No. 21;  
Matches 35; Conservative 11; Mismatches 25; Indels 60; Gaps 9;  
QY 20 RGICVPCQINRVGS-----VTNAG---DLATLAT 45  
DB 78 RDRCLPCNCKSKSLARCDNSGRCSCKEYTGARCDRLCPGFHLITDAGCTDDQLNLS 137  
QY 46 QCSCTGPTGALDDGVTVDFDRSAQCVCXKCP-----NFTYN--GSGPQGEARG 92  
DB 138 KCDCCD-PAGIA---GPCD-----AGRCV-CKPAVTGBCDRCRSGYVNLDDGNPBCG--C 184  
QY 93 VQVFMAAAMAA 103  
DB 185 TQCFVGHSHS 195  
RESULT 11  
MMSA  
laminin alpha-1 chain precursor - mouse  
N:Alternate names: laminin chain A1  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 09-Jul-2004  
C:Accession: A31771; A30449; S00624; A30450; S08895; S02578; S01790; A30451; S14670  
R:Sasaki, M.; Kleitman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.  
J. Biol. Chem. 263, 16536-16544, 1988  
A:Title: Laminin, a multidomain protein. The A chain has a unique globular domain and ho  
A:Reference number: A31771; MUID:89034134; PMID:3182802  
A:Accession: A31771  
A:Molecule type: mRNA  
A:Residues: 1-3084 <SAS>  
A:Cross-references: UNIPROT:P19137; UNIPARC:UPI00000278CA; EMBL:J04064; NID:g309419; PID  
A:Accession: A30449  
A:Molecule type: protein

A:Residues: 183-195, 570-571, 'A', 573-586, 596-612, 'X', 614-617, 'EMK', 630-646, 1217-1222, 'YF  
2486; 2624-2639; 2818-2843; 3009-3033, 'V', 3035 <SA2>  
A:Cross-references: UNIPARC:UPI0000173C92; UNIPARC:UPI0000173C93; UNIPARC:UPI0000173C94;  
C99; UNIPARC:UPI0000173CA3; UNIPARC:UPI0000173C99; UNIPARC:UPI0000173C9C; UNIPARC:UPI000  
10000173CA2  
R:Harti, L.; Oberbauer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A:Title: The N terminus of laminin A chain is homologous to the B chain.  
A:Reference number: S00624; MUID:88225080; PMID:3267223  
A:Accession: S00624  
A:Molecule type: mRNA  
A:Residues: 1-208, 'T', 210-334 <HAR>  
A:Cross-references: UNIPARC:UPI000016CE8F; EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID  
A:Accession: A30450  
A:Molecule type: protein  
A:Residues: 311-335, 'N', 337-339, 630-642, 'D', 644, 692-734, 737-748, 'X', 750-760, 'G', 762-763,  
3-1389, 1449-1459 <HAR2>  
A:Cross-references: UNIPARC:UPI0000173CA3; UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CA5,  
CA4; UNIPARC:UPI0000173CAB; UNIPARC:UPI0000173CAC  
A:Note: The sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-11e  
R:Mann, K.; Deutzmann, R.; Timpl, R.  
Eur. J. Biochem. 178, 71-80, 1988  
A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th  
A:Reference number: S08895; MUID:89078415; PMID:2462498  
A:Accession: S08895  
A:Molecule type: protein  
A:Residues: 153-169 <MAN>  
A:Cross-references: UNIPARC:UPI0000173CAD  
R:Fujitawa, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 252, 453-461, 1988  
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A:Reference number: S02678; MUID:88326259; PMID:2458101  
A:Accession: S02678  
A:Molecule type: protein  
A:Residues: 630-642, 'D', 644, 2690-2704 <FUV>  
A:Cross-references: UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CAE  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Harti, L.  
Eur. J. Biochem. 177, 35-45, 1988  
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te  
A:Reference number: S01790; MUID:89030693; PMID:3181157  
A:Accession: S01790  
A:Molecule type: mRNA  
A:Residues: 2538-3084 <DEU>  
A:Cross-references: UNIPARC:UPI000016C8E; EMBL:X13459; NID:g55499; PIDN:CAA31807.1; PID  
A:Accession: A30451  
A:Molecule type: protein  
A:Residues: 1911-1929, 1997-2006, 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105, 2120  
470; 2487-2498; 2502-2525; 2538-2557; 2561-2591, 'X', 2593-2594; 2600-2610; 2616-2645; 2648-2655,  
93; 2998-3005, 'A', 3007-3033, 'V', 3035; 3068-3083 <DE2>  
A:Cross-references: UNIPARC:UPI0000173CB6; UNIPARC:UPI0000173CB7; UNIPARC:UPI0000173CB8,  
CB7; UNIPARC:UPI0000173CB; UNIPARC:UPI0000173CBF; UNIPARC:UPI0000173CC0; UNIPARC:UPI000  
10000173CC6; UNIPARC:UPI0000173CC7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CC9; UNIPAR  
A:Note: 2256-Val was also found  
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
Lab. Invest. 60, 772-782, 1989  
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A:Reference number: A34961; MUID:89280632; PMID:2733383  
A:Accession: S14670  
A:Molecule type: protein  
A:Residues: 2424-2436, 2440-2451, 2461-2467, 2487-2525, 2550-2557, 2561-2593, 2600-2610, 2616-2  
-2942, 'T', 2944-2964; 2969-2976; 2980-2993; 2998-3000, 'I', 3002-3018, 'V', 3020-3034; 3068-3083  
A:Cross-references: UNIPARC:UPI0000173CB9; UNIPARC:UPI0000173CAE; UNIPARC:UPI0000173CB,  
CC7; UNIPARC:UPI0000173CB; UNIPARC:UPI0000173CCA; UNIPARC:UPI0000173CB; UNIPARC:UPI000  
10000173CD1; UNIPARC:UPI0000173CD2; UNIPARC:UPI0000173CD3; UNIPARC:UPI0000173CD4; UNIPAR  
C/Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
A:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-24/Domain: signal sequence #status predicted <Sig>  
F:25-3084/Product: laminin alpha-1 chain #status predicted <MAT>  
F:25-277/Domain: VI <DOM6>  
F:277-331/Domain: laminin-type EGF-like homology <LE01>



F/278-519/Domain: V <DOM5>  
F/334-401/Domain: laminin-type EGF-like homology <LE02>  
F/404-458/Domain: laminin-type EGF-like homology <LE03>  
F/461-507/Domain: laminin-type EGF-like homology <LE04>  
F/510-519/Domain: laminin-type EGF-like homology <LE05>  
F/520-515/Domain: IYD <DO4B>  
F/716-1166/Domain: IYD <DO3B>  
F/716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F/749-795/Domain: laminin-type EGF-like homology <LE07>  
F/798-853/Domain: laminin-type EGF-like homology <LE08>  
F/830-834/Region: cell adhesion #status predicted  
F/856-906/Domain: laminin-type EGF-like homology <LE09>  
F/909-955/Domain: laminin-type EGF-like homology <LE10>  
F/958-1002/Domain: laminin-type EGF-like homology <LE11>  
F/1005-1048/Domain: laminin-type EGF-like homology <LE12>  
F/1051-1094/Domain: laminin-type EGF-like homology <LE13>  
F/1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>  
F/1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>  
F/1147-1149/Region: cell attachment (R-G-D) motif  
F/1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>  
F/1167-1368/Domain: IVA <DO4A>  
F/1369-1561/Domain: IIR <DO3A>  
F/1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>  
F/1410-1466/Domain: laminin-type EGF-like homology <LE18>  
F/1459-1513/Domain: laminin-type EGF-like homology <LE19>  
F/1516-1560/Domain: laminin-type EGF-like homology <LE20>  
F/1562-2133/Domain: IYI <DOM2>  
F/1562-2133/Region: heptad repeats  
F/2134-3084/Domain: G <DOM3>  
F/2150-2308/Domain: laminin G repeat homology <LG1>  
F/2137-2452/Domain: laminin G repeat homology <LG2>  
F/2218-2683/Domain: laminin G repeat homology <LG3>  
F/2418-2897/Domain: laminin G repeat homology <LG4>  
F/2925-3082/Domain: laminin G repeat homology <LG5>  
F/25/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted  
F/45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718  
e (Asn) (covalent) #status predicted  
F/304-312/Diulfide bonds: #status experimental  
F/770,857,1997,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status absent  
F/845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 13.4%; Score 75; DB 1; Length 3084;  
Best Local Similarity 30.0%; Pred. No. 52;  
Matches 21; Conservative 10; Mismatches 31; Indels 8; Gaps 2;  
Db 23 CVCQIRVGSVTNAGDLATATQCTGCTGALDGVTFDRSAQCVCCKP-NFY 81  
1094 CVCQCDLRLPTCLPCTCLGGLCSGSDSGCKENVV-----GPGCKQAGTFAL 1146  
QY 82 NGSPQGEAP 91  
Db 1147 RGDNPQGCSP 1156

RESULT 12  
S24802  
polyferredoxin 6x2[4Fe-4S] vhub [similarity] - Methanococcus voltae  
C/Species: Methanococcus voltae  
C/Date: 10-Sep-1999 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: S24802  
R/Halboch, S.; Klein, A.  
submitted to the EMBL Data Library, August 1991  
A/Title: Methanococcus voltae harbors two gene groups each of homologous (NiFe) - a  
A/Reference number: S16721  
A/Accession: S24802  
A/Molecule type: DNA  
A/Residues: 1-398 <HAL>  
A/Cross-references: UNIPROT:Q00388; UNIPARC:UP100000629BE; EMBL:X61204; NID:G1747406; PI  
A/Experimental source: Strain PS(DSM1537)  
R/Halboch, S.; Klein, A.  
Mol. Gen. Genet. 233, 217-224, 1992  
A/Title: Methanococcus voltae harbors four gene clusters potentially encoding two (NiFe)  
A/Reference number: A59304; MUID:92293118; PMID:1603063

A/Contents: annotation  
C/Genetics:  
A/Name: vhub  
C/Superfamily: polyferredoxin 6x2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology  
F/4-52/Domain: ferredoxin 2[4Fe-4S] homology <FER1>  
F/56-109/Domain: ferredoxin 2[4Fe-4S] homology <FER2>  
F/125-179/Domain: ferredoxin 2[4Fe-4S] homology <FER3>  
F/192-247/Domain: ferredoxin 2[4Fe-4S] homology <FER4>  
F/261-329/Domain: ferredoxin 2[4Fe-4S] homology <FER5>  
F/341-395/Domain: ferredoxin 2[4Fe-4S] homology <FER6>

Query Match 13.0%; Score 72.5; DB 1; Length 398;  
Best Local Similarity 27.6%; Pred. No. 13;  
Matches 16; Conservative 13; Mismatches 22; Indels 7; Gaps 2;  
Db 23 CVCQIRVGSVTNAGDLA-----TLATQCTGCTGALDGVTFDRSAQCVCCK 75  
11 CLVCMNSKACPELEIAIPFKTCLCFSCASACPGALVENNKLIYNS--KCIKC 66  
RESULT 13  
T26063  
hypothetical protein W01F3.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T26063  
R/Cummings, P.  
submitted to the EMBL Data Library, March 1997  
A/Reference number: Z20145  
A/Accession: T26063  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-2225 <WIL>  
A/Cross-references: UNIPROT:Q045881; UNIPARC:UP100000816EC; EMBL:Z92815; PTDN:CAB07294.1  
A/Experimental source: clone W01F3  
C/Genetics:  
A/Gene: CBSP.W01F3.3  
A/Map position: 5  
A/Insertions: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1

Query Match 13.0%; Score 72.5; DB 2; Length 2225;  
Best Local Similarity 28.3%; Pred. No. 67;  
Matches 28; Conservative 11; Mismatches 41; Indels 19; Gaps 4;  
Db 8 NGSPFANANAGICVPCQ--INRVGSVTNAGDLATATQCT-----QCPTG 54  
1862 DGN-----ANNF--GSLDDCQLCVLINQSIKNGKVAATTAPQITPEEEKLAPGCPG 1915  
QY 55 TALDDGVTFDRSAQCVCCKRNFYNGSPQGEAPGV 93  
Db 1916 RAPLGSSPYLCCGNSAESICPTSYCCRRGPPDVCCPGV 1954  
RESULT 14  
S18323  
thyroglobulin - bullfrog  
C/Species: Rana catesbeiana (bullfrog)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S18323  
R/Hayashi, H.; Omiya, Y.; Suzuki, S.  
FEBS Lett. 292, 168-170, 1991  
A/Title: Thyroglobulin in bullfrog thyroglobulin is a thyroid hormone generating site.  
A/Reference number: S18323; MUID:92070481; PMID:1959601  
A/Accession: S18323  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-109 <HAY>  
A/Cross-references: UNIPROT:Q7LZ58; UNIPARC:UP10000179E77

```

QY      12 PFAANNARGICVPCQINRVSVTNAGDLATLATQCTGTCTALDDGVTVDFDRSAQ 71
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      32 PSAVXQASLKLIL-SRADLIGNVAGCG-----ICPVGSSESDG-----E 69
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      72 CVKCKPNFYNGSGPQG--EAPGVQ 94
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      70 CVPCPHGFYQYKTSPPGMYOKPGVE 94
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

## RESULT 15

```

JC7530
Vascular apoptosis-inducing protein 1 - western diamondback rattlesnake
C:Species: Crotalus atrox (western diamondback rattlesnake)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7530; PC7105
R;Maeda, S.; Ohta, T.; Kaji, K.; Fox, J.W.; Hayashi, H.; Araki, S.
Biochem. Biophys. Res. Commun. 278, 197-204, 2000
A>Title: CDNA cloning and characterization of vascular apoptosis-inducing protein 1.
A:Reference number: JC7530; MUID:20525424; PMID:11071872
A:Contents: Crude venom gland
A:Accession: JC7530
A:Molecule type: mRNA
A:Residues: 1-610 <MAS>
A:Cross-references: UNIPROT:Q9DGB9; UNIPARC:UPI00000FC726; DDBJ:AB042840
A:Accession: PC7105
A:Molecule type: protein
A:Residues: 240-251; 274-283; 378-385; 507-519 <MA2>
A:Cross-references: UNIPARC:UPI0000178FAE; UNIPARC:UPI0000178FAP; UNIPARC:UPI0000178FBO;
C:Comment: This protein, as a homodimeric protein, belongs to snake venom metalloproteas
a specific substrate, induces apoptosis in vascular endothelial cells.
C:Genetics:
A:Gene: VAP1
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: apoptosis

```

```

Query Match      12.7%; Score 71; DB 2; Length 610;
Best Local Similarity 26.7%; Pred. No. 28;
Matches 24; Conservative 11; Mismatches 39; Indels 16; Gaps 4;

```

```

QY      19 ARGICV-PCQINRVSVTNAG----DLATLATQCTGTCTALDDGVTVDFDRSAQCV 73
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      444 AEGLCDDQCFKAGAGTECRPAKDECDWADVCTGRSAEC-----IDRFQNGQPC- 492
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      74 KCKPNFYNGSGPQGEAPGVQVPAAGAAA 103
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB      493 KNNNGCYNCKPCIMADQCIALFGPGATVS 522
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Search completed: December 5, 2005, 06:17:54  
Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 5, 2005, 05:59:29 ; Search time 188 Seconds

(without alignments)  
245.398 Million cell updates/sec

Title: US-09-196-161D-1

Perfect score: 558  
Sequence: 1 GAAAGCANQNPFAANNANAR.....PGSEAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: geneseqp19808.\*  
2: geneseqp19908.\*  
3: geneseqp20008.\*  
4: geneseqp20018.\*  
5: geneseqp20028.\*  
6: geneseqp20038.\*  
7: geneseqp20048.\*  
8: geneseqp20058.\*  
9: geneseqp20068.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	409	3 AAB25889	Aab25889 IAG48 (GI
2	558	100.0	442	3 AAY97176	Aay97176 48 kDa Im
3	558	100.0	442	3 AAB25859	Aab25859 48KD 1-an
4	558	100.0	442	9 Adz67374	Adz67374 Ichthyoph
5	297	53.2	89	3 AAB25862	Aab25862 48KD 1-an
6	261	46.2	83	3 AAB25861	Aab25861 48KD 1-an
7	261	46.2	89	3 AAB25863	Aab25863 48KD 1-an
8	221	39.6	468	3 AAY97177	Aay97177 55 kDa Im
9	221	39.6	468	3 AAB25882	Aab25882 Synthetic
10	221	39.6	468	3 AAB25860	Aab25860 55KD 1-an
11	221	39.6	468	9 Adz67375	Adz67375 Ichthyoph
12	139	24.9	76	3 AAB25885	Aab25885 55KD 1-an
13	119	21.3	69	3 AAB25864	Aab25864 48KD 1-an
14	102	18.3	72	3 AAB25888	Aab25888 55KD 1-an
15	91	16.3	1755	8 ADP31446	Adp31446 Human sec
16	89	15.9	72	3 AAB25865	Aab25865 48KD 1-an
17	86	15.4	1464	8 ADP31437	Adp31437 Human sec
18	85.5	15.3	1076	6 ABU6845	Abu6845 Human PRO
19	85.5	15.3	1076	6 ABU6845	Abu6845 Human PRO
20	84.5	15.1	1450	8 ADO01059	Ado01059 Mouse hom
21	84.5	15.1	1737	8 ADO01057	Ado01057 Human hom
22	84.5	15.1	1774	5 ABG6800	Abg6800 Human REM
23	84.5	15.1	2789	7 ADC51660	Adc51660 Human MEG
24	84.5	15.1	2789	7 ADG75733	Adg75733 Human pro

25	84.5	15.1	2854	5 ADH48732	Adh48732 NOV7 prot
26	84	15.1	613	2 AAW73009	Aaw73009 Cobra ven
27	84	15.1	621	2 AAW73013	Aaw73013 Cobra ven
28	83.5	15.0	70	3 AAB25887	Aab25887 55KD 1-an
29	83.5	15.0	7339	6 AAO16358	Aao16358 Human tra
30	83	14.9	13	3 AAB25898	Aab25898 Ichthyoph
31	83	14.9	70	3 AAB25884	Aab25884 55KD 1-an
32	83	14.9	1390	6 ADA74091	Ada74091 Equine 1a
33	83	14.9	1849	8 ADP30752	Adp30752 Human sec
34	82	14.7	472	8 ADP31222	Adp31222 Human sec
35	82	14.7	750	8 ADP31131	Adp31131 Human sec
36	81.5	14.6	464	9 AEA42406	Aea42406 Immunogen
37	81.5	14.6	525	8 ADP31227	Adp31227 Human sec
38	80.5	14.4	261	6 ABU21604	Abu21604 Protein e
39	80.5	14.4	1587	8 ADP30579	Adp30579 Human sec
40	80	14.3	267	9 ADZ47919	Adz47919 Araf-1CAR
41	80	14.3	320	8 ADP31607	Adp31607 Human sec
42	80	14.3	320	8 ADP31649	Adp31649 Human sec
43	79.5	14.2	531	8 ADP31696	Adp31696 Human sec
44	79	14.2	337	8 ADP31387	Adp31387 Human sec
45	79	14.2	2440	9 AEB79086	Aeb79086 Mouse lam

## ALIGNMENTS

RESULT 1	
AAB25889	
ID AAB25889 standard; protein; 409 AA.	
XX	
AC AAB25889;	
XX	
DT 18-DEC-2000 (first entry)	
XX	
DE IAG48 (GI) surface protein amino acid sequence.	
XX	
KM Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;	
KW white spot disease; freshwater fish; immune response; infection control.	
OS Ichthyophthirius multifiliis.	
XX	
PN WO200046373-A1.	
XX	
PD 10-AUG-2000.	
XX	
PF 04-FEB-2000; 2000MO-US002962.	
XX	
PR 04-FEB-1999; 99US-0118634P.	
PR 02-MAR-1999; 99US-012372P.	
PR 17-MAR-1999; 99US-0124905P.	
PR 27-APR-1999; 99US-0131121P.	
XX	
PA (UYGE-) UNIV GEORGIA RES FOUND INC.	
PA (CORR ) CORNELL RES FOUND INC.	
PA (CLAR/) CLARK T G.	
PA (DICK/) DICKERSON H W.	
PA (LINT/) LIN T.	
XX	
PI Clark TG, Dickerson HW, Lin T;	
PI WPI; 2000-506071/45.	
DR	
XX	
PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius	
PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius	
PT infection in fish.	
XX	
PS Disclosure; Fig 8; 144p; English.	
XX	
CC This invention relates to novel i-antigen polypeptide sequences. I-	
CC antigens or immobilisation antigens are common to a variety of	
CC hymenostomacid ciliates and their expression varies in response to	
CC environmental stimuli. This invention relates to i-antigen in	
CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite	

of freshwater fish causing ichthyophthiriasis or white spot disease. The invention includes two polypeptide and polynucleotide sequences for two i-antigens, of 48 and 55 KD. Also included in the invention are antibodies capable of binding to the nucleotide sequences and a method for identifying I. multifiliis serotypes using the nucleotide sequences. A composition (containing the i-antigen nucleotide) capable of eliciting an immune response in fish is useful for prophylaxis, treatment or for controlling I. multifiliis infection in fish. Polynucleotide or protein vaccines comprising a portion of the amplified product encoding an antigenic i-antigen polypeptide obtained is also useful for treating or preventing I. multifiliis infection in fish. Sequences AA97036-A97042, and AA97060, AA97065 and AA97089 represent i-antigen genes and gene fragments identified in the invention. Sequences AA97043-A97064 (excluding AA97060) and AA97071-A97088 represent primers used in the isolation of the i-antigen gene sequences. Sequences AA825839-B25889 and AA825893-B25906 represent i-antigen protein and peptide sequences

	Query Match	100.0%	Score 558	DB 3	Length 409
	Best Local Similarity	100.0%	Pred. No. 4.6e-51		
	Matches 105	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 GAAGGANGNPFAANNAARGICVFCQINRRGVTNAGDLATLATQCTGCTGPTGALDDG	60			
Db	37 GAAOGEANGNPFAANNAARGICVFCQINRRGVTNAGDLATLATQCTGCTGPTGALDDG	96			
QY	61 VTDFVDRSAACVCKPFFYNGSGPOEARGVQVFAAGAAAGV	105			
Db	97 VTDFVDRSAACVCKPFFYNGSGPOEARGVQVFAAGAAAGV	141			

RESULT 2  
AA97176  
ID AA97176 standard; protein; 442 AA.

AC	AA97176;	
XX		
DT	06-AUG-2003	(revised)
DT	04-DEC-2000	(first entry)
XX		
DE	48 kDa	immobilization-antigen

KM BTII, beta-tubulin, protein expression system, negative selection,  
KM paciferael sensitivity, cell surface, antigen, protozoa, ciliate,  
KM live vaccine, Ichthyophthirius multifiliis, immobilization-antigen,  
KM I-antigen, freshwater, fish, protozoacide.

XX  
OS Ichthyophichthys multifiliis.

	Location/Qualifiers
Key	1. .442
FH	
FT	
FT	/note= "Gln encoded by CAR, TAG or TAA"

PN WO200046381-A1.

PD 10-AUG-2000.

AA  
PF 04-FEB-2000; 2000WO-US002966.

XX	04-FEB-1999;	99US-0118634P
PR	02-MAR-1999;	99US-0122372P
PR	17-MAR-1999;	99US-0124905P
PR	27-APR-1999;	99US-0131121P

PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (GAER/) GAERTIG J.  
PA (DICK/) DICKERSON H W.  
PA (CLAR/) CLARK T G.

GAERTIG J, DICKERSON HW, CLARK TG,  
WPI; 2000-514962/46.

DR N-PSDB: AAA52134, AAA52135.  
XX  
XX Recombinant expression systems for expressing heterologous nucleic acids  
FI and producing recombinant protein, comprises nonpathogenic protozoa such  
PT as *Tetrahymena* resistant to pactitaxel.  
XX  
XX  
PS Disclosure: Fig 3A; 83pp; English.

Tetrahymena thermophila expresses two major beta-tubulin genes (BTU1 and BTU2), which encode identical beta-tubulin proteins. Either of these two genes (but not both at once) can be disrupted without a detectable change in the cell phenotype. A K350L substitution in the BTU1 beta-tubulin protein confers increased resistance to microtubule-depolymerizing drugs and increased sensitivity to paclitaxel, a microtubule-stabilizing drug. Cells carrying the Btut1-K350M allele can be transformed to paclitaxel resistance by gene replacement of Btut1-K350M with a wild-type Btut1 gene fragment, eliminating the need to incorporate a means for positive selection. Where the host organism is not a T. thermophila mutant containing the Btut1-K350M allele, Btut1::neo construct, which substitutes the coding region of the neo gene (conferring resistance to paromomycin) for that of Btut1, can be used to generate Btut1 gene knockouts and for positive selection. Heterologous nucleic acids (especially encoding antigenic polypeptides) can be inserted into a Btut1 gene for successful cell-surface expression that is maintained by way of negative selection. Preferred expression vectors disrupt the Btut1-K350M gene by homologous recombination-mediated insertion of a heterologous nucleic acid, thereby restoring resistance to paclitaxel in the resulting transgenic host. Transgenic ciliated protozoa are useful as live vaccines for stimulating an immune response in a vertebrate. The transgenic protozoan host cells are also useful for producing polyclonal antibodies (claimed). In particular, Tetrahymena expressing Ichthyophthirius multifiliis immobilization-antigen (I antigen) protein on their surface are effective vehicles for vaccination of freshwater fish against infection by I. multifiliis. (Updated on 06-AUG-2003 to correct OS field.)

AA Sequence 442 AA;  
SQ

Query Match	100.0%;	Score 558;	DB 3;	Length 442;
Best Local Similarity	100.0%;	Pred. No. 5,1e-51;		
Matches 105; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 GAAGGAAAGNGDPEAANNARAGTCAVCCGICNRVGSATNAGLATLTATCCGCTCCPGTGLTDDG 60  
 |||  
 Db 56 GAAGGAAAGNGDPEAANNARAGTCAVCCGICNRVGSATNAGLATLTATCCGCTCCPGTGLTDDG 115  
 |||  
 QY 61 VTDAFDRSAACVCCKKPNFYNGSSPQGEAPGVQVFAAGAAAGV 105  
 |||  
 Db 116 VTDAFDRSAACVCCKKPNFYNGSSPQGEAPGVQVFAAGAAAGV 160  
 |||

RESULT 3  
AAB25859  
ID AAB25859 standard; protein; 442 AA.

AC AAB25859;

DT 18-DEC-2000 (first entry)

48kD i-antigen protein sequence.

XX Ichthyophthirius multifiliis.

PN WO200046373-A1.

AS PD 10-AUG-2000.

04-FEB-2000; 2000WO-US002962.

04-FEB-1999; 99US-0118634P.

PR 02-MAR-1999; 99US-0122372P.  
 PR 17-MAR-1999; 99US-0124905P.  
 PR 27-APR-1999; 99US-0131121P.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA (CORR.) CORNELL RES FOUND INC.  
 PA (CLAR/) CLARK T G.  
 PA (DICK/) DICKERSON H W.  
 PA (LINT/) LINT T.  
 XX  
 PI Clark TG, Dickerson HW, Lin T;  
 XX  
 DR WPI; 2000-506071/45.  
 XX  
 PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius  
 PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius  
 PT infection in fish.  
 XX  
 PS Claim 1; Fig 1; 144pp; English.  
 XX  
 CC This invention relates to novel i-antigen polypeptide sequences. I-  
 CC antigens or immobilisation antigens are common to a variety of  
 CC hymenocometid ciliates and their expression varies in response to  
 CC environmental stimuli. This invention relates to i-antigens in  
 CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite  
 CC of freshwater fish causing ichthyophthiriasis or white spot disease. The  
 CC invention includes two polypeptide and polynucleotide sequences for two i-  
 CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies  
 CC capable of binding to the nucleotide sequences and a method for  
 CC identifying i. multifiliis serotypes using the nucleotide sequences. A  
 CC composition (containing the i-antigen nucleotide) capable of eliciting an  
 CC immune response in fish is useful for prophylaxis, treatment or for  
 CC controlling i. multifiliis infection in fish. Polynucleotide or protein  
 CC vaccines comprising a portion of the amplified product encoding an  
 CC antigenic i-antigen polypeptide obtained is also useful for treating or  
 CC preventing i. multifiliis infection in fish. Sequences AAA97036-A97042,  
 CC and AAA97060, AAA97065 and AAA97089 represent i-antigen genes and gene  
 CC fragments identified in the invention. Sequences AAA97043-A97064  
 CC (including AAA97060) and AAA97071-A97088 represent primers used in the  
 CC isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and  
 CC AAB25893-B25906 represent i-antigen protein and peptide sequences  
 XX  
 SQ Sequence 442 AA;  
 Query Match 100.0%; Score 558; DB 3; Length 442;  
 Best Local Similarity 100.0%; Pred. No.5.1e-51;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 60  
 DB 56 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 115  
 QY 61 VTDVFDPSAAQCVKCKPFFYNGSSPQGEAPGVQVFAAGAAAGV 105  
 DB 116 VTDVFDPSAAQCVKCKPFFYNGSSPQGEAPGVQVFAAGAAAGV 160  
 RESULT 4  
 AAB25862  
 ID AAB25862 standard; protein; 442 AA.  
 XX  
 AC AAB25862;  
 XX  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Ichthyophthirius multifiliis 48 kD antigen protein.  
 XX  
 KM cloning; protozoacide; vaccine; recombinant polypeptides; protozoa;  
 KM ciliate; transgenic cell.  
 XX  
 OS Ichthyophthirius multifiliis.  
 XX  
 PN US2005106164-A1.

XX  
 XX 19-MAY-2005.  
 PD  
 XX  
 PF 28-JUN-2004; 2004US-00878694.  
 XX  
 PR 04-FEB-1999; 99US-0118634P.  
 PR 02-MAR-1999; 99US-0122372P.  
 PR 17-MAR-1999; 99US-0124905P.  
 PR 27-APR-1999; 99US-0131121P.  
 PR 04-FEB-2000; 2000US-00498612.  
 XX  
 PA (GAER/) GAERTIG J.  
 PA (DICK/) DICKERSON H W.  
 PA (CLAR/) CLARK T G.  
 PA (CASS/) CASSIDY-HANLEY D.  
 XX  
 PI Gaertig J, Dickerson HW, Clark TG, Cassidy-Hanley D;  
 XX  
 DR WPI; 2005-354778/36.  
 XX  
 PT Producing recombinant polypeptides in Tetrahymena by transforming  
 PT Tetrahymena cells with a nucleic acid encoding a recombinant polypeptide,  
 PT useful as live vaccines for freshwater fish against infection by  
 PT Ichthyophthirius multifiliis.  
 XX  
 PS Disclosure; SEQ ID NO 5; 66pp; English.  
 XX  
 CC The invention relates to a method of producing (M1) recombinant  
 CC polypeptides (1) in Tetrahymena comprising transforming Tetrahymena cells  
 CC with a nucleic acid that encodes a recombinant polypeptide comprising a  
 CC vertebrate polypeptide, culturing the transformed Tetrahymena cells to  
 CC produce the recombinant polypeptide, and isolating the recombinant  
 CC polypeptide. The methods and compositions of the present invention are  
 CC useful in the field of recombinant protein production, particularly  
 CC recombinant protein production in non-pathogenic protozoa, such as the  
 CC ciliate Tetrahymena, and for producing live vaccines for freshwater fish  
 CC against infection by Ichthyophthirius multifiliis. The transgenic cells  
 CC may also be used to isolate and purify antibodies. This sequence  
 CC corresponds to the protein sequence of the Ichthyophthirius multifiliis  
 CC 48 kD antigen used in the method of the invention.  
 XX  
 SQ Sequence 442 AA;  
 Query Match 100.0%; Score 558; DB 9; Length 442;  
 Best Local Similarity 100.0%; Pred. No.5.1e-51;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 60  
 DB 56 GAAOGEANGNPPAANNAARGICVPCQINRVGSVTNAGDLATLATGCTGCTGTALDDG 115  
 QY 61 VTDVFDPSAAQCVKCKPFFYNGSSPQGEAPGVQVFAAGAAAGV 105  
 DB 116 VTDVFDPSAAQCVKCKPFFYNGSSPQGEAPGVQVFAAGAAAGV 160  
 RESULT 5  
 AAB25862  
 ID AAB25862 standard; protein; 89 AA.  
 XX  
 AC AAB25862;  
 XX  
 DT 18-DEC-2000 (first entry)  
 XX  
 DE 48kD i-antigen repeat amino acid sequence SEQ ID 9.  
 XX  
 KM Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine;  
 KM white spot disease; freshwater fish; immune response; infection control.  
 XX  
 OS Ichthyophthirius multifiliis.  
 XX  
 PN WO200046373-A1.

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PD 10-AUG-2000.
XX
XX 04-FEB-2000; 2000MO-US002962.
XX
PR 04-FEB-1999; 99US-0118634P.
XX 02-MAR-1999; 99US-0122372P.
PR 17-MAR-1999; 99US-0124905P.
XX 27-APR-1999; 99US-0131121P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (CORR) CORNELL RES FOUND INC.
PA (CLAR/) CLARK T G.
PA (DICK/) DICKERSON H W.
XX (LINT/) LIN T.
XX
PI Clark TG, Dickerson HW, Lin T;
XX WPI, 2000-506071/45.
XX
PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
XX multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
XX infection in fish.
XX
XX Disclosure; Fig 5a; 144pp; English.
XX
XX This invention relates to novel i-antigen polypeptide sequences. I-
XX antigens or immobilisation antigens are common to a variety of
XX CC hymenostomatid ciliates and their expression varies in response to
XX CC environmental stimuli. This invention relates to i-antigens in
XX CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
XX CC of freshwater fish causing ichthyophthiriasis or white spot disease. The
XX CC invention includes two polypeptide and polynucleotide sequences for two i
XX CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
XX CC capable of binding to the nucleotide sequences and a method for
XX CC identifying i. multifiliis serotypes using the nucleotide sequences. A
XX CC composition (containing the i-antigen nucleotide) capable of eliciting an
XX CC immune response in fish is useful for prophylaxis, treatment or for
XX CC controlling i. multifiliis infection in fish. Polynucleotide or protein
XX CC vaccines comprising a portion of the amplified product encoding an
XX CC antigenic i-antigen polypeptide obtained is also useful for treating or
XX CC preventing i. multifiliis infection in fish. Sequences AA97036-A97042,
XX CC and AA97060, AA97065 and AA97089 represent i-antigen genes and gene
XX CC fragments identified in the invention. Sequences AA97043-A97064
XX CC (excluding AA97060) and AA97071-A97088 represent primers used in the
XX CC isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and
XX CC AAB25893-B25906 represent i-antigen protein and peptide sequences
XX
XX SQ Sequence 89 AA;
XX
XX Query Match 53.2%; Score 297; DB 3; Length 89;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-24;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 51 CPTGTLADGVTVDVFDPSAAQCVCXKPNFYNGSGSQGEAPGVQVFAAGAAAGV 105
XX |||||
XX 1 CPTGTLADGVTVDVFDPSAAQCVCXKPNFYNGSGSQGEAPGVQVFAAGAAAGV 55
XX
XX Db
XX
XX RESULT 6
XX AAB25861
XX ID AAB25861 standard; protein; 83 AA.
XX
XX AC AAB25861;
XX
XX DT 18-DEC-2000 (first entry)
XX
XX 48kD i-antigen repeat amino acid sequence SEQ ID 8.
XX
XX DE Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
XX KM white spot disease; freshwater fish; immune response; infection control.
XX OS Ichthyophthirius multifiliis.
XX

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PN WO200046373-A1.
XX
XX 10-AUG-2000.
XX
XX 04-FEB-2000; 2000MO-US002962.
XX
XX 04-FEB-1999; 99US-0118634P.
XX 02-MAR-1999; 99US-0122372P.
PR 17-MAR-1999; 99US-0124905P.
XX 27-APR-1999; 99US-0131121P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (CORR) CORNELL RES FOUND INC.
PA (CLAR/) CLARK T G.
PA (DICK/) DICKERSON H W.
XX (LINT/) LIN T.
XX
XX Clark TG, Dickerson HW, Lin T;
XX WPI, 2000-506071/45.
XX
XX Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius
XX multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
XX infection in fish.
XX
XX Disclosure; Fig 5a; 144pp; English.
XX
XX This invention relates to novel i-antigen polypeptide sequences. I-
XX antigens or immobilisation antigens are common to a variety of
XX CC hymenostomatid ciliates and their expression varies in response to
XX CC environmental stimuli. This invention relates to i-antigens in
XX CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite
XX CC of freshwater fish causing ichthyophthiriasis or white spot disease. The
XX CC invention includes two polypeptide and polynucleotide sequences for two i
XX CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies
XX CC capable of binding to the nucleotide sequences and a method for
XX CC identifying i. multifiliis serotypes using the nucleotide sequences. A
XX CC composition (containing the i-antigen nucleotide) capable of eliciting an
XX CC immune response in fish is useful for prophylaxis, treatment or for
XX CC controlling i. multifiliis infection in fish. Polynucleotide or protein
XX CC vaccines comprising a portion of the amplified product encoding an
XX CC antigenic i-antigen polypeptide obtained is also useful for treating or
XX CC preventing i. multifiliis infection in fish. Sequences AA97036-A97042,
XX CC and AA97060, AA97065 and AA97089 represent i-antigen genes and gene
XX CC fragments identified in the invention. Sequences AA97043-A97064
XX CC (excluding AA97060) and AA97071-A97088 represent primers used in the
XX CC isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and
XX CC AAB25893-B25906 represent i-antigen protein and peptide sequences
XX
XX SQ Sequence 83 AA;
XX
XX Query Match 46.8%; Score 261; DB 3; Length 83;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-20;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAQGEANGNQPFPAANNAARGICVPCQINRVGSVTNAGDLATATQCSQ 50
XX |||||
XX 34 GAAQGEANGNQPFPAANNAARGICVPCQINRVGSVTNAGDLATATQCSQ 83
XX
XX Db
XX
XX RESULT 7
XX AAB25863
XX ID AAB25863 standard; protein; 89 AA.
XX
XX AC AAB25863;
XX
XX DT 18-DEC-2000 (first entry)
XX
XX 48kD i-antigen repeat amino acid sequence SEQ ID 10.
XX
XX DE Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;
XX KM white spot disease; freshwater fish; immune response; infection control.
XX OS
XX

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OS Ichthyophthirius multifiliis.  
 XX MO200046373-A1.  
 XX  
 XX  
 PD 10-AUG-2000.  
 XX  
 PF 04-FEB-2000; 2000MO-US002962.  
 XX  
 PR 04-FEB-1999; 99US-0118634P.  
 PR 02-MAR-1999; 99US-0122372P.  
 PR 17-MAR-1999; 99US-0124905P.  
 PR 27-APR-1999; 99US-0131121P.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA (CORR ) CORNELL RES FOUND INC.  
 PA (CLAR/) CLARK T G.  
 PA (DICK/) DICKERSON H W.  
 PA (LINT/) LIN T.  
 PI CLARK TG, Dickerson HW, Lin T;  
 DR WPI; 2000-506071/45.  
 XX  
 PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius  
 PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius  
 PT infection in fish.  
 XX  
 PS Disclosure; Fig 5a; 14pp; English.  
 XX  
 CC This invention relates to novel i-antigen polypeptide sequences. I-  
 CC antigens or immobilization antigens are common to a variety of  
 CC hymenostemal ciliates and their expression varies in response to  
 CC environmental stimuli. This invention relates to i-antigens in  
 CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite  
 CC of freshwater fish causing ichthyophthiriasis or white spot disease. The  
 CC invention includes two polypeptide and polynucleotide sequences for two i  
 CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies  
 CC capable of binding to the nucleotide sequences and a method for  
 CC identifying i. multifiliis serotypes using the nucleotide sequences. A  
 CC composition (containing the i-antigen nucleotide) capable of eliciting an  
 CC immune response in fish is useful for prophylaxis, treatment or for  
 CC controlling i. multifiliis infection in fish. Polynucleotide or protein  
 CC vaccines comprising a portion of the amplified product encoding an  
 CC vaccine i-antigen polypeptide obtained is also useful for treating or  
 CC preventing i. multifiliis infection in fish. Sequences AAA97036-A97042,  
 CC and AAA97060, AAA97065 and AAA97089 represent i-antigen genes and gene  
 CC fragments identified in the invention. Sequences AAA97043-A97064  
 CC (excluding AAA97060) and AAA97071-A97088 represent primers used in the  
 CC isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and  
 CC AAB25893-B25906 represent i-antigen protein and peptide sequences  
 XX  
 SQ Sequence 89 AA;  
 Query Match 46.2%; Score 258; DB 3; Length 89;  
 Best Local Similarity 87.3%; Pred. No. 1,1e-19;  
 Matches 46; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 51 CPTGTALDDGVTDVFDRAAQCVCCKNPFYNGSGPGGAAGVGVFAAGAAAGV 105  
 DB 1 CPTGTALDDGVTDVFDRAAQCVCCKNPFYNGSGPGGAAGVGVFAAGAAAGV 55  
 RESULT 8  
 AAY97177  
 ID AAY97177 standard; protein; 468 AA.  
 XX  
 AC AAY97177;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE 55 kDa immobilization antigen.  
 XX

KW BTU1, beta-tubulin; protein expression system; negative selection;  
 KW pacitaxel sensitivity; cell surface; antigen; protozoa; ciliate;  
 KW live vaccine; Ichthyophthirius multifiliis; immobilization-antigen;  
 KW i-antigen; freshwater; fish; protozoacide.  
 XX  
 OS Ichthyophthirius multifiliis.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..468 "Gln encoded by CAR or TAA"  
 FT /note="Gln encoded by CAR or TAA"  
 XX  
 PN MO200046381-A1.  
 XX  
 PD 10-AUG-2000.  
 XX  
 PF 04-FEB-2000; 2000MO-US002966.  
 XX  
 PR 04-FEB-1999; 99US-0118634P.  
 PR 02-MAR-1999; 99US-0122372P.  
 PR 17-MAR-1999; 99US-0124905P.  
 PR 27-APR-1999; 99US-0131121P.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA (GAER/) GAERTIG J.  
 PA (DICK/) DICKERSON H W.  
 PA (CLAR/) CLARK T G.  
 PI Gaertig J, Dickerson HW, Clark TG;  
 PT  
 PT WPI; 2000-514962/46.  
 DR N-PSDB; AAA52136.  
 XX  
 PT Recombinant expression systems for expressing heterologous nucleic acids  
 PT and producing recombinant protein, comprises nonpathogenic protozoa such  
 PT as Tetrahymena resistant to pacitaxel.  
 XX  
 PS Disclosure; Fig 3a; 83pp; English.  
 XX  
 CC Tetrahymena thermophila expresses two major beta-tubulin genes (BTU1 and  
 CC BTU2), which encode identical beta-tubulin proteins. Either of these two  
 CC genes (but not both at once) can be disrupted without a detectable change  
 CC in the cell phenotype. A K350L substitution in the BTU1 beta-tubulin  
 CC protein confers increased resistance to microtubule-depolymerizing drugs  
 CC and increased sensitivity to pacitaxel, a microtubule-stabilizing drug.  
 CC Cells carrying the Btu1-K350M allele can be transformed to pacitaxel  
 CC resistance by gene replacement of Btu1-K350M with a wild-type BTU1 gene  
 CC fragment, eliminating the need to incorporate a means for positive  
 CC selection. Where the host organism is not a T. thermophila mutant  
 CC containing the Btu1-K350M allele, BTU1::neol construct, which  
 CC substitutes the coding region of the neol gene (conferring resistance to  
 CC paromycin) for that of BTU1, can be used to generate BTU1 gene knockouts  
 CC and for positive selection. Heterologous nucleic acids (especially  
 CC encoding antigenic polypeptides) can be inserted into a BTU1 gene for  
 CC successful cell-surface expression that is maintained by way of negative  
 CC selection. Preferred expression vectors disrupt the Btu1-K350M gene by  
 CC homologous recombination-mediated insertion of a heterologous nucleic  
 CC acid, thereby restoring resistance to pacitaxel in the resulting  
 CC transgenic host. Transgenic ciliated protozoa are useful as live vaccines  
 CC for stimulating an immune response in a vertebrate. The transgenic  
 CC protozoan host cells are also useful for producing polyclonal antibodies  
 CC (claimed). In particular, Tetrahymena expressing Ichthyophthirius  
 CC multifiliis immobilization-antigen (i-antigen) protein on their surface  
 CC are effective vehicles for vaccination of freshwater fish against  
 CC infection by i. multifiliis. (Updated on 06-AUG-2003 to correct OS  
 CC field.)  
 XX  
 SQ Sequence 468 AA;  
 Query Match 39.6%; Score 221; DB 3; Length 468;  
 Best Local Similarity 53.3%; Pred. No. 6.6e-15;  
 Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;  
 QY 17 NAARGIVPCQINRVGVTNAGDLATLATGCTGCTGTALDDGVTDVFDRAAQCVCCK 76

DB 131 NAGASTCTACPVNRVGALTAGNAATIVAGCNVACPTGTALDDGVTDDVRSFTCEVKCR 190  
QY 77 PNFYNGSGSPGCEAP 91  
DB 191 LNFYNGNN--GNTP 203

RESULT 9  
AAB25882  
ID AAB25882 standard; protein; 468 AA.  
XX  
AC AAB25882;  
XX  
DT 18-DEC-2000 (first entry)  
XX  
DE Synthetic 55kd i-antigen protein L6P.  
XX  
KM Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;  
KM white spot disease; freshwater fish; immune response; infection control.  
XX  
OS Ichthyophthirius multifiliis.  
OS Synthetic.  
XX  
PN WO200046373-A1.  
XX  
PD 10-AUG-2000.  
XX  
PF 04-FEB-2000; 2000MO-US002962.  
XX  
PR 04-FEB-1999; 99US-0118634P.  
PR 02-MAR-1999; 99US-0122372P.  
PR 17-MAR-1999; 99US-0124905P.  
PR 27-APR-1999; 99US-0131121P.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (CORR) CORNELL RES FOUND INC.  
PA (CLAR/) CLARK T G.  
PA (DICK/) DICKERSON H W.  
PA (LINT/) LIN T.  
PI Clark TG, Dickerson HW, Lin T;  
PI MPI; 2000-506071/45.  
PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius  
PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius  
PT infection in fish.  
XX  
PS Example 5; Fig 14; 144p; English.  
XX  
CC This invention relates to novel i-antigen polypeptide sequences. I-  
CC antigens or immobilisation antigens are common to a variety of  
CC hymenostomatid ciliates and their expression varies in response to  
CC environmental stimuli. This invention relates to i-antigens in  
CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite  
CC of freshwater fish causing ichthyophthiriasis or white spot disease. The  
CC invention includes two polypeptide and polynucleotide sequences for two i-  
CC antigens, of 48 and 55 kD. Also included in the invention are antibodies  
CC capable of binding to the nucleotide sequences and a method for  
CC identifying i. multifiliis serotypes using the nucleotide sequences. A  
CC composition (containing the i-antigen nucleotide) capable of eliciting an  
CC immune response in fish is useful for prophylaxis, treatment or for  
CC controlling i. multifiliis infection in fish. Polynucleotide or protein  
CC vaccines comprising a portion of the amplified product encoding an  
CC antigenic i-antigen polypeptide obtained is also useful for treating or  
CC preventing i. multifiliis infection in fish. Sequences AAB25882-597042,  
CC and AAB25882-597045 and AAB25882-597048 represent i-antigen genes and gene  
CC fragments identified in the invention. Sequences AAB25882-597043-597044  
CC (excluding AAB25882-597045) and AAB25882-597048 represent primers used in the  
CC isolation of the i-antigen gene sequences. Sequences AAB25882-597042 and  
CC AAB25882-597045 represent i-antigen protein and peptide sequences  
XX

SQ Sequence 468 AA;  
Query Match 39.6%; Score 221; DB 3; Length 468;  
Best Local Similarity 53.3%; Pred. No. 6, 6e-15;  
Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;

QY 17 NARGICVPCQINRVGSVTNAGDLATLTAQCSGCTGTALDDGVTDDVRSAAQCCKK 76  
DB 131 NAGASTCTACPVNRVGALTAGNAATIVAGCNVACPTGTALDDGVTDDVRSFTCEVKCR 190  
QY 77 PNFYNGSGSPGCEAP 91  
DB 191 LNFYNGNN--GNTP 203

RESULT 10  
AAB25860  
ID AAB25860 standard; protein; 468 AA.  
XX  
AC AAB25860;  
XX  
DT 18-DEC-2000 (first entry)  
XX  
DE 55kd i-antigen protein of parasite isolate G5.  
XX  
KM Immobilisation antigen; i-antigen; Ichthyophthiriasis; vaccine;  
KM white spot disease; freshwater fish; immune response; infection control.  
XX  
OS Ichthyophthirius multifiliis.  
XX  
PN WO200046373-A1.  
XX  
PD 10-AUG-2000.  
XX  
PF 04-FEB-2000; 2000MO-US002962.  
XX  
PR 04-FEB-1999; 99US-0118634P.  
PR 02-MAR-1999; 99US-0122372P.  
PR 17-MAR-1999; 99US-0124905P.  
PR 27-APR-1999; 99US-0131121P.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (CORR) CORNELL RES FOUND INC.  
PA (CLAR/) CLARK T G.  
PA (DICK/) DICKERSON H W.  
PA (LINT/) LIN T.  
PI Clark TG, Dickerson HW, Lin T;  
PI MPI; 2000-506071/45.  
PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius  
PT multifiliis, useful for prophylaxis and treatment of Ichthyophthirius  
PT infection in fish.  
XX  
PS Claim 3; Fig 3; 144p; English.  
XX  
CC This invention relates to novel i-antigen polypeptide sequences. I-  
CC antigens or immobilisation antigens are common to a variety of  
CC hymenostomatid ciliates and their expression varies in response to  
CC environmental stimuli. This invention relates to i-antigens in  
CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite  
CC of freshwater fish causing ichthyophthiriasis or white spot disease. The  
CC invention includes two polypeptide and polynucleotide sequences for two i-  
CC antigens, of 48 and 55 kD. Also included in the invention are antibodies  
CC capable of binding to the nucleotide sequences and a method for  
CC identifying i. multifiliis serotypes using the nucleotide sequences. A  
CC composition (containing the i-antigen nucleotide) capable of eliciting an  
CC immune response in fish is useful for prophylaxis, treatment or for  
CC controlling i. multifiliis infection in fish. Polynucleotide or protein  
CC vaccines comprising a portion of the amplified product encoding an  
CC antigenic i-antigen polypeptide obtained is also useful for treating or  
CC preventing i. multifiliis infection in fish. Sequences AAB25860-597042,  
CC



CC and AAB25885 and AAB25885 represent i-antigen genes and gene  
CC fragments identified in the invention. Sequences AAB25885-897064  
CC (excluding AAB25885) and AAB25885-897064 represent primers used in the  
CC isolation of the i-antigen gene sequences. Sequences AAB25885-897064  
CC AAB25885-897064 represent i-antigen protein and peptide sequences  
XX  
SQ Sequence 468 AA;  
Query Match 39.6%; Score 221; DB 3; Length 468;  
Best Local Similarity 53.3%; Pred. No. 6.6e-15;  
Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;  
QY 17 NAARGICVPCQINRVGSVTNAGDLATLTCGTCPTGTALDGDGTVDFDRSAACVCKK 76  
DB 131 NAGASTCTACPVNRVGALTAGNAATTVAGCNVACPTGTALDGDGTVDFDRSAACVCKK 190  
QY 77 PNFFYNGSGSPQGEAP 91  
DB 191 LNFFYNGNN--GNTP 203  
RESULT 11  
AD267375  
ID AD267375 standard; protein; 468 AA.  
XX  
AC AD267375;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
DE Ichthyophthirius multifiliis 55 kD antigen protein.  
XX  
KM cloning; protozoacide; vaccine; recombinant polypeptides; protozoa;  
XX ciliate; transgenic cell.  
XX  
OS Ichthyophthirius multifiliis.  
XX  
PN US2005106164-A1.  
XX  
PD 19-MAY-2005.  
XX  
PF 28-JUN-2004; 2004US-00878694.  
XX  
PR 04-FEB-1999; 99US-0118634P.  
XX 02-MAR-1999; 99US-0122372P.  
XX 17-MAR-1999; 99US-0124905P.  
XX 27-APR-1999; 99US-0131121P.  
XX 04-FEB-2000; 2000US-00498612.  
XX  
PA (GABR/) GAERTIG J.  
PA (DICK/) DICKERSON H W.  
PA (CLAR/) CLARK T G.  
PA (CASS/) CASSIDY-HANLEY D.  
XX  
PI Gaertig J, Dickerson HW, Clark TG, Cassidy-Hanley D;  
XX WPI, 2005-354778/36.  
XX  
DR WPI, 2005-354778/36.  
XX  
PT Producing recombinant polypeptides in Tetrahymena by transforming  
XX Tetrahymena cells with a nucleic acid encoding a recombinant polypeptide,  
PT useful as live vaccines for freshwater fish against infection by  
XX Ichthyophthirius multifiliis.  
XX  
PS Disclosure; SEQ ID NO 6; 66pp; English.  
XX  
CC The invention relates to a method of producing (M1) recombinant  
CC polypeptides (I) in Tetrahymena comprising transforming Tetrahymena cells  
CC with a nucleic acid that encodes a recombinant polypeptide comprising a  
CC vertebrate polypeptide, culturing the transformed Tetrahymena cells to  
CC produce the recombinant polypeptide, and isolating the recombinant  
CC polypeptide. The methods and compositions of the present invention are  
CC useful in the field of recombinant protein production, particularly  
CC recombinant protein production in non-pathogenic protozoa, such as the  
CC ciliate Tetrahymena, and for producing live vaccines for freshwater fish

CC against infection by Ichthyophthirius multifiliis. The transgenic cells  
CC may also be used to isolate and purify antibodies. This sequence  
CC corresponds to the protein sequence of the Ichthyophthirius multifiliis  
CC 55 kD antigen used in the method of the invention.  
XX  
SQ Sequence 468 AA;  
Query Match 39.6%; Score 221; DB 9; Length 468;  
Best Local Similarity 53.3%; Pred. No. 6.6e-15;  
Matches 40; Conservative 8; Mismatches 25; Indels 2; Gaps 1;  
QY 17 NAARGICVPCQINRVGSVTNAGDLATLTCGTCPTGTALDGDGTVDFDRSAACVCKK 76  
DB 131 NAGASTCTACPVNRVGALTAGNAATTVAGCNVACPTGTALDGDGTVDFDRSAACVCKK 190  
QY 77 PNFFYNGSGSPQGEAP 91  
DB 191 LNFFYNGNN--GNTP 203  
RESULT 12  
AAB25885  
ID AAB25885 standard; peptide; 76 AA.  
XX  
AC AAB25885;  
XX  
DT 18-DEC-2000 (first entry)  
XX  
DE 55kD i-antigen amino acid repeat sequence SEQ ID 57.  
XX  
KM Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine;  
XX white spot disease; freshwater fish; immune response; infection control.  
XX  
OS Ichthyophthirius multifiliis.  
XX  
PN WO2000046373-A1.  
XX  
PD 10-AUG-2000.  
XX  
PF 04-FEB-2000; 2000WO-US002962.  
XX  
PR 04-FEB-1999; 99US-0118634P.  
XX 02-MAR-1999; 99US-0122372P.  
XX 17-MAR-1999; 99US-0124905P.  
XX 27-APR-1999; 99US-0131121P.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (CORR) CORNELL RES FOUND INC.  
PA (CLAR/) CLARK T G.  
PA (DICK/) DICKERSON H W.  
PA (LINT/) LINT T.  
XX  
PI Clark TG, Dickerson HW, Lin T;  
XX WPI, 2000-506071/45.  
XX  
DR WPI, 2000-506071/45.  
XX  
PT Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius  
XX multifiliis, useful for prophylaxis and treatment of Ichthyophthirius  
XX infection in fish.  
XX  
PS Disclosure; Fig 5b; 14pp; English.  
XX  
CC This invention relates to novel i-antigen polypeptide sequences. I-  
CC antigens or immobilisation antigens are common to a variety of  
CC hymenostomatid ciliates and their expression varies in response to  
CC environmental stimuli. This invention relates to i-antigens in  
CC Ichthyophthirius multifiliis, a protozoan which is an obligate parasite  
CC of freshwater fish causing ichthyophthiriosis or white spot disease. The  
CC invention includes two polypeptide and polynucleotide sequences for two i-  
CC antigens, of 48 and 55 kD. Also included in the invention are antibodies  
CC capable of binding to the nucleotide sequences and a method for  
CC identifying i. multifiliis serotypes using the nucleotide sequences. A  
CC composition (containing the i-antigen nucleotide) capable of eliciting an



CC -antigens, of 48 and 55 kD. Also included in the invention are antibodies  
CC capable of binding to the nucleotide sequences and a method for  
CC identifying I. multificilis serotypes using the nucleotide sequences. A  
CC composition (containing the I-antigen nucleotide) capable of eliciting an  
CC immune response in fish is useful for prophylaxis, treatment or for  
CC controlling I. multificilis infection in fish. Polynucleotide or protein  
CC vaccines comprising a portion of the amplified product encoding an  
CC antigenic I-antigen polypeptide obtained is also useful for treating or  
CC preventing I. multificilis infection in fish. Sequences AAA97036-A97042,  
CC and AAA97060, AAA97065 and AAA97089 represent I-antigen genes and gene  
CC fragments identified in the invention. Sequences AAA97043-A97064  
CC (excluding AAA97060) and AAA97071-A97088 represent primers used in the  
CC isolation of the I-antigen gene sequences. Sequences AAB25859-B25889 and  
CC AAB25893-B25906 represent I-antigen protein and peptide sequences  
XX  
SQ Sequence 72 AA;  
  
Query Match 18.3%; Score 102; DB 3; Length 72;  
Best Local Similarity 53.3%; Pred. No. 0.0042; 9; Mismatches 0;  
Matches 16; Conservative 5; Indels 0; Gaps 0;  
  
OY 51 CPTGTALDDGVTDFDRSAACVCCKPNFY 80  
||| ||| ||| : ||| ||| |||  
1 CPAGTIVLTGTTSTYKQAASECVCANFY 30  
Db  
  
RESULT 15  
ADP31446  
ID ADP31446 standard; protein; 1755 AA.  
XX  
AC ADP31446;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
XX Human secreted protein SEQ ID #2213.  
DE  
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN MO2004035732-A2.  
XX  
XX  
PD 29-APR-2004.  
XX  
XX  
PF 28-AUG-2003; 2003MO-US026780.  
XX  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.

PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485225P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kochakota S, Haisan L, Linnemann T;  
PI Pierre K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
XX WPI; 2004-348438/32.  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
XX Claim 1; SEQ ID NO 3444; 428pp; English.  
XX  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOMB and is not in the specification.  
XX  
XX  
SQ Sequence 1755 AA;  
  
Query Match 16.3%; Score 91; DB 8; Length 1755;  
Best Local Similarity 34.6%; Pred. No. 2.5;  
Matches 36; Conservative 2; Mismatches 48; Indels 18; Gaps 5;  
  
OY 1 GAAQGANNGNPANNAARGICVPCOINRVGSVTNAGDLATLATCGTCPTGTALDDG 60

Db 1472 GAAAGAAAGAAAAA--CAAGCTACACTACACCTGGTCAT--TACATTCATATTGGAG 1527  
Qy 61 VTDFDRSNAQCCKKPNFYNGSPQGEAPGVVPAAGAAAG 104  
Db 1528 A-----AATCCAGCTG---TAGCCCAAGG---AAGAGAG 1557

Search completed: December 5, 2005, 06:02:47  
Job time : 191 secs

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OM protein - protein search, using SW model

Run on: December 5, 2005, 06:16:28 ; Search time 15 seconds  
(without alignment)  
33.518 Million cell updates/sec

Title: US-09-196-161D-1

Sequence: 1 GAAGGAGNNGPFAANNAR.....PGGAPGVVFAAGAAAGV 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep: \*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep: \*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep: \*  
5: /cgn2\_6/ptodata/2/pubpaa/PC7\_NEW\_PUB pep: \*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep: \*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep: \*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85.5	15.3	1076	US-10-131-826A-219	Sequence 219, App
2	72.5	13.0	913	US-10-821-234-1040	Sequence 1040, Ap
3	72.5	13.0	3717	US-10-821-234-1076	Sequence 1076, Ap
4	72	12.9	468	US-11-076-187-2	Sequence 2, Appl
5	69.5	12.5	544	US-10-980-388-40	Sequence 40, Appl
6	69	12.4	396	US-10-467-657-280	Sequence 280, App
7	69	12.4	396	US-10-467-657-4380	Sequence 4380, App
8	68.5	12.3	415	US-11-182-946-6	Sequence 6, Appl
9	68.5	12.3	750	US-11-132-285-2	Sequence 2, Appl
10	68.5	12.3	1001	US-11-132-285-40	Sequence 40, Appl
11	68.5	12.3	1013	US-10-131-826A-38	Sequence 38, Appl
12	67	12.0	334	US-10-514-057-6	Sequence 6, Appl
13	67	12.0	335	US-11-182-946-7	Sequence 7, Appl
14	67	12.0	669	US-11-076-187-3	Sequence 3, Appl
15	65	11.6	354	US-10-478-345-2	Sequence 2, Appl
16	64.5	11.6	353	US-10-131-826A-296	Sequence 296, App
17	63.5	11.4	820	US-10-467-657-4910	Sequence 4910, Appl
18	63	11.3	1042	US-11-067-811-1	Sequence 1, Appl
19	62.5	11.2	354	US-10-467-657-6058	Sequence 6058, App
20	62.5	11.2	993	US-11-137-465-36	Sequence 36, Appl
21	60.5	10.8	321	US-10-478-345-8	Sequence 8, Appl
22	60.5	10.8	4419	US-10-821-234-1155	Sequence 1155, Ap
23	60	10.8	3500	US-11-085-775-2	Sequence 2, Appl
24	59	10.6	483	US-10-467-657-2774	Sequence 2774, Ap
25	58.5	10.5	964	US-11-137-465-58	Sequence 58, Appl

ALIGNMENTS

26	58.5	10.5	965	7	US-11-113-424-2	Sequence 2, Appl
27	58.5	10.5	965	7	US-11-147-047-51	Sequence 51, Appl
28	58	10.4	251	7	US-11-054-515-1219	Sequence 1219, Ap
29	58	10.4	575	6	US-10-980-388-46	Sequence 46, Appl
30	57.5	10.3	248	7	US-11-080-628-23	Sequence 23, Appl
31	57.5	10.3	7968	7	US-11-186-731-5	Sequence 5, Appl
32	57	10.2	961	7	US-11-113-424-35	Sequence 35, Appl
33	56.5	10.1	228	6	US-10-980-388-17	Sequence 17, Appl
34	56.5	10.1	357	6	US-10-478-345-6	Sequence 6, Appl
35	56.5	10.1	359	7	US-11-105-172-2	Sequence 340, Appl
36	56.5	10.1	386	6	US-10-131-826A-340	Sequence 320, App
37	56	10.0	250	6	US-10-131-826A-330	Sequence 11, Appl
38	56	10.0	255	7	US-11-182-946-11	Sequence 3516, App
39	56	10.0	395	6	US-10-467-657-3516	Sequence 46, Appl
40	56	10.0	493	7	US-11-137-465-46	Sequence 35, Appl
41	56	10.0	897	7	US-11-137-465-35	Sequence 84, Appl
42	56	10.0	2004	6	US-10-467-657-84	Sequence 6322, Ap
43	56	10.0	2004	6	US-10-467-657-6322	Sequence 1116, Ap
44	56	10.0	5405	7	US-11-108-172-1116	Sequence 2075, Ap
45	55.5	9.9	246	7	US-11-054-515-2075	

RESULT 1  
US-10-131-826A-219  
; Sequence 219, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Guirney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P9330R1C128  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.



```
RESULT 5
US-10-980-388-40
; Sequence 40, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,860
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-40

Query Match          12.5%; Score 69.5; DB 6; Length 544;
Best Local Similarity 25.7%; Pred. No. 1.2; Indels 23; Gaps 3;
Matches 28; Conservative 3; Mismatches 55;

QY 1 GAAQGEANGNQPPAANNAAGICVPCQINRVGSVTNAGDIATLATQCSCTCPTGTALDDG 60
Db 403 GATTTCTGTATTCTTCATACCACTGTTATG---ATAATCTTACAGTAAGAT 458
QY 61 VTDFPDR-----SAAQCCKKPNFYNGSSPQGEAPGVQVFAAGAAAG 104
Db 459 TTTTCTTAGCTAAACAC-----AACCTATAAAATTTG 493

RESULT 6
US-10-467-657-280
; Sequence 280, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
```

```
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Segwin99, version 1.04
; SEQ ID NO 280
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-280

Query Match          12.4%; Score 69; DB 6; Length 396;
Best Local Similarity 22.5%; Pred. No. 0.94; Indels 20; Gaps 2;
Matches 18; Conservative 12; Mismatches 30;

QY 25 PCQINRVGSVTNAGDIATLATQCSCTCPTGTALDDGVTVFDRSAQCCKKPNFYNGG 84
Db 311 PCQI-----CTHCCPVQALAPBG--DIHPNCTICLHCQVMYHDDR 350
QY 85 SPQGEAPGVQVFAAGAAAG 104
Db 351 CPQVVAENKKQKQAAAKSG 370

RESULT 7
US-10-467-657-4380
; Sequence 4380, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Segwin99, version 1.04
; SEQ ID NO 4380
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4380

Query Match          12.4%; Score 69; DB 6; Length 396;
Best Local Similarity 22.5%; Pred. No. 0.94; Indels 20; Gaps 2;
Matches 18; Conservative 12; Mismatches 30;

QY 25 PCQINRVGSVTNAGDIATLATQCSCTCPTGTALDDGVTVFDRSAQCCKKPNFYNGG 84
Db 311 PCQI-----CTHCCPVQALAPBG--DIHPNCTICLHCQVMYHDDR 350
QY 85 SPQGEAPGVQVFAAGAAAG 104
Db 351 CPQVVAENKKQKQAAAKSG 370

RESULT 8
US-11-182-946-6
; Sequence 6, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
```

```

CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US/10/186,643
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US/09/573,986
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-11-182-946-6

Query Match      12.3%; Score 68.5; DB 7; Length 415;
Best Local Similarity    27.7%; Pred.No. 1.1;
Matches   18; Conservative     6; Mismatches    22; Indels    19; Gaps    2

OY          23 CVCQINVGASVTNAGDLATLATGCGTCTGTALDDGVTVDFDRSAACVCKKPNFYXN 82
           |||::|||-----VLCPETAE--VTDEIMTDVNCVCKRGRHON 179
DB          139 CVHCEREL-----

OY          83 GGSPQ 87
           |||
DB         180 TSSPR 184

RESULT 9
US-11-132-285-2
Sequence 2, Application US/1132285
Publication No. US20050244876A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
FILE REFERENCE: PF511P1
CURRENT APPLICATION NUMBER: US/11/132,285
CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: US/10/046,433
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/261,960
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/618,570
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/144,087
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 60/149,450
PRIOR FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: 60/149,712
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/153,089
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 750
TYPE: PRT
ORGANISM: Homo sapiens
US-11-132-285-2

Query Match      12.3%; Score 68.5; DB 7; Length 750;
Best Local Similarity    23.6%; Pred.No. 2.1;
Matches   17; Conservative     7; Mismatches    29; Indels    19; Gaps    3

OY          17 NARGICVCCQINRVGSVTNAGDLATLATGCGTCTGTALDDGVTVDFDRSAACVKCK 76
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB          331 NGVASLCRCAL-----EADSVGCC-TSCAGIYT-----DROSGTCNSCP 371
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY          77 PNFFYNNGSPPQG 88
           |||
DB         372 PWTLKAHQPYG 383

RESULT 10
US-11-132-285-40
```

```

; Sequence 40 Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-132-285-40

Query Match      12.3% Score 68.5; DB 7; Length 1001;
Best Local Similarity 23.6%; Pred. No. 2.9;
Matches 17; Conservative 7; Mismatches 29; Indels 19; Gaps 3

QY      17 NANGICVPCQINVGSVTNAGDLATATGCGTCGTGALDDGVTVDVDSAAQCVRCK 76
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      582 NGVASVYCRPAL-----EASDVGSSC-TSCPAGYI-----DRDSGTCHSCP 622

QY      77 PNFYNGGSPQG 88
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      623 PNTLKAHPYG 634

RESULT 11
US-10-131-826A-38
; Sequence 38, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974

```



```

; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 38
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 877, 882
; OTHER INFORMATION: unknown amino acid
US-10-131-826A-38
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```

Query Match          12.3%; Score 68.5; DB 6; Length 1013;
Best Local Similarity 23.6%; Pred. No. 2.9;
Matches 17; Conservative 7; Mismatches 29; Indels 19; Gaps 3;
```

```
Qy      17  NAARGICVPCQINRVGSVTNAGDLATLATQCSCTQCPGTALDDGVTVDFRSAACVCKK 76
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      582  NGVASYRCPAL-----EASDVGSSC-TSCPGAYI-----DRDSGTCHSCP 622
```

```
Qy      77  PNFRYNGGSPQG 88
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      623  PNILKAQPYG 634
```

```

RESULT 12
US-10-514-057-6
; Sequence 6, Application US/10514057
; Publication No. US20050255547A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; TITLE OF INVENTION: Novel hexamers of receptors, members of the TNF-receptor family,
; TITLE OF INVENTION: their use in therapy and pharmaceutical compositions comprising
; FILE REFERENCE: 11436*15
; CURRENT APPLICATION NUMBER: US/10/514,057
; PRIOR APPLICATION NUMBER: PCT/EP02/12186
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: PCT/EP02/05103
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-514-057-6
```

```

Query Match          12.0%; Score 67; DB 6; Length 334;
Best Local Similarity 26.7%; Pred. No. 1.3;
Matches 20; Conservative 12; Mismatches 29; Indels 14; Gaps 4;
```

```

Qy      8  NGNOPFANNARGICVPCQINRVGSVTNAGDLATLATQCSCTQCPGTALDDGVTVDFR 67
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      98  NGDEP-----DCVPCQEGK--EYTDKAFSSKRCRCRL-CDEGHGLEVEIN--CTR 143
```

```
Qy      68  SAAQCVCKRPNFYNN 82
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      144  TONTKCRCKPNFFCN 158
```

```

RESULT 13
US-11-182-946-7
; Sequence 7, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-7
```

```

Query Match          12.0%; Score 67; DB 7; Length 335;
Best Local Similarity 26.7%; Pred. No. 1.3;
Matches 20; Conservative 12; Mismatches 29; Indels 14; Gaps 4;
```

```
Qy      8  NGNOPFANNARGICVPCQINRVGSVTNAGDLATLATQCSCTQCPGTALDDGVTVDFR 67
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      76  NGDEP-----DCVPCQEGK--EYTDKAFSSKRCRCRL-CDEGHGLEVEIN--CTR 121
```

```
Qy      68  SAAQCVCKRPNFYNN 82
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      122  TONTKCRCKPNFFCN 136
```

```

RESULT 14
US-11-076-187-3
; Sequence 3, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF355P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
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/ PRIOR APPLICATION NUMBER: 60/413,861
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: 10/648,786
/ PRIOR FILING DATE: 2003-08-27
/ PRIOR APPLICATION NUMBER: 60/551,768
/ PRIOR FILING DATE: 2004-03-11
/ PRIOR APPLICATION NUMBER: 60/608,469
/ PRIOR FILING DATE: 2004-09-10
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 3
/ LENGTH: 669
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-076-187-3
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Query Match          12.0%; Score 67; DB 7; Length 669;
Best Local Similarity 26.7%; Pred. No. 2.7;
Matches 20; Conservative 12; Mismatches 29; Indels 14; Gaps 4;
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```
QY      8  NGNQPFAANNAGICVPCQINRVGSVTNAGDLATLATGCGPTGTALDDGVTVDFDR 67
DB      76  NGDEP-----DCVPCQEGK-EYTDKAHFSSKRCRCL-CDGSHGLEVEIN--CTR 121
QY      68  SAAQCVCKCKNFYYN 82
DB      122  TQNTKCRCKNPFQCN 136
```

```
RESULT 15
US-10-478-345-2
/ Sequence 2, Application US/10478345
/ Publication No. US20050255115A1
/ GENERAL INFORMATION:
/ APPLICANT: Institute of Genetics and Devel. Biol, CAS
/ APPLICANT: Dongguan HaoFa Biotechnology Developmental Co., Ltd.
/ APPLICANT: Beijing ABT Genetic Engineering Technology Co., Ltd.
/ TITLE OF INVENTION: Anti Human Ovarian Cancer- Anti CD3 Bispecific Antibody
/ FILE REFERENCE: L53-2-11393-US01
/ CURRENT APPLICATION NUMBER: US/10/478,345
/ PRIOR FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: CN 0118247.4
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: PCT/CN02/00347
/ PRIOR FILING DATE: 2002-05-23
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 354
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: AA Seq of VH against human ovarian cancer
US-10-478-345-2
```

```
Query Match          11.6%; Score 65; DB 6; Length 354;
Best Local Similarity 25.2%; Pred. No. 2.2;
Matches 29; Conservative 3; Mismatches 43; Indels 40; Gaps 5;
```

```
QY      1  GAAQGEANGNQPFANNAGICVPCQINRVGSVTNAGDLATLATGCGPTGTALDDG 60
DB      44  GAGAGACAGT---CAGATCTCTGCAAGGCTTCTGGG---TATACCTTC----- 87
QY      61  VTDFVDRSAAQCVCKCKNFYYNGSPG-----EAPGVQVFAAGAAAG 104
DB      88  -----ACAACTGC-----TGGAATGCAGTGGGTGCAGAAAGATGCCAGGAAAG 129
```

Search completed: December 5, 2005, 06:21:26  
Job time : 16 secs